	COCCENTORIC GICAACCANG TODACCGICA CCACGGACTG ATCAACAAGT TOSCAGGCGA	60
	COCCOCCTO GCCATCTTCG GAGCCCCGAA CCGCCTCGAC CGTCCCGAAG ACQCCGCGCT	120
	SCOUCESC COGCCATAN CCCANOSCUT GCCNACGAS ATMOCCGAGG TCCAAGCCGG	180
	CATCGGGGTG GCGGCAGGGC ANATCGTCGC CGGCAATGTC GGCGCCAAGC AAAGATTONA	240
5	ATACACASTO GYOGGAAGO COGTCAACCA NGCGGCCCGA TTGTGCGAAC TGGCCAAATC	300
	ACACCCCECE CORTTEGETC TYGCCCGCTC GGCTYATGGT CACCCAATTY AAGGACTACT	350
	TYGGCCTGGC GCACGACCTG CCGAAGTGGG CGACTGAAGG CGCCAAAGCC GCCGTTGAGG	420
	COSCOARGO GTTGCOGGCC GCCGTTCCGG CCATTCCGRS TGCTGGCCTC ASCGGCGTTG	486
	CHURCHCOST CARICARDOS GOSTOROTOS GURGATTERA GUTTOCOGOC GUSTOGACON	540
10	OCACGACCC GOCGGCGAGC CCCGCGGTGC TGCCGGCGTC CAACGGCCTC GGAGCCGCGG	600
	CONCONCTUA AGGITOGAÇA CACGOGITTG GOGGGATGCO GCTCATGGGI AMOGGTGCOG	650
	DACGRECOTT TRACARCTIC GCTGCCCCTC GRTACGGATT CARGCCGACC GRGATOGCCC	720
	AACCGCCGGC TGGCGGATGA CCRACTECTT TOSTTSATCS ASSATCSAAT TCHACGATTC	780
	AAAGGGAGGA ATTCATATGA CCTCNOWTT TATGACGGAT CCGCACGCNA TNEGGGACAT	840
15	COCCOCCET TTTGAGGTCC ACCCCCAGAC GGTGERAGGAC GAGGCTEGCE GGATGTGGGC	900
20	OTCCOCOCAA AACATTTCCC GTOCOGGCTG GACTOGCATG GCCCAGGCCGA CCTCCNTACA	960
	CACCATEGOC CAGATGANTO AGGOSTITON CAACATOOTS AACATSCISC ACSESSIONS	1020
	TEACGGGCTG GTTCGCGACG CCRACACTA CGAACAGCAA GAGCAGGCCT CCCAGCAGCAGT	1080
	COTCASCAGE TGACCOGGC CGACGACTCA GGAGGACACA TGACCATCAA CTATCAATTC	1140
20	GOOGACCTOG ACCOCCATGO OCCURTANTO COCCUPTES COGGGTTGCT GEAGGCCGAG	1390
600	CAPCAGGCCA TCATFTCTGA TGTGTTGACC GCGAGTGACT TTTGGGGCGG CGCCGGTTCG	1260
	GOSGOCTGCC ASSIGNTCAT TACCCAGTTG GGCCDTAACT TCCAGGTGAT TTACGAGCAG	1326
		1380
	GCCARCGCCC ACGGGCAGAA GGTGCAGGCT GCCGGCAACA ACATGGCACA AASCGACAACA	1440
25	SCOSTNOSNI CERGETOGGE CIRACCOGGG TENTAAGTIG GGTCCGCGCA GGGCGGGCCG	
20	ATCAGOSTEG ACTITOGOGO COGATACACO GOCATETTET REFUSGGAAC ACVGUGUUG	1500
	CETCAENTOC COCCTTCCCC TTGTTNGGCB ACGTGCTCGG TGATGGCTTT GACGACCCCT	1550
	TORCORROR GROCANTONA TERRESCUE TERRENTAR COCRTTOTTE CUACCOCCOC	1420
	GGOGCOGCGA GYTGYCCCYY GAAATAAGGA AYYACAGCAC GOGCGAACAG CYCAYAGGAG	1680
20	TERRAGETIC COUNSCOUR SCUC	1704
30		
	(2) INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 2286 base pairs	
35	(B) TYPE: nucleic scid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40		
	(xi: SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	COSTOTTEGO STOTEGGOGO ATTSTEATOT SEGCOANTIS COCCITODACO CAGACOSCUC	50
	CCAGCTTOTC GATCCAGOCC GOGACCOGGA TTGCCACCGC GCGAACCGGG AACGGATTCT	120
45	COUCTURATT CIGOGICACI TONCAGNOGO GOOGIGAIC CHUITUGONA NCAGCGICIG	1.80
	GAACGGGCUT CHAACGCGTU UCGTAAGCCC AGCUTGTACG CCGTCAGCCC GACGCCGATG	249
	CCGAATGCCT TOCCGCCCAA GCTGAGCCGC GCGGGCTCCA CCAAGAGCGT CACGGTGAGC	390
	CAGCCAACCA GATGCAACCC CACGATCACC GCGAACTGCC GAATTCGCCA CGAGAGGTGC	359
	TGGAAATCCA GCAATACGCC CGCGAGCCGA TCTCGTTGGA CCAGACCATC GGCGACGAGG	429
50	GOGACAGNICA GCTTGGCGAT TTCATCGAAA ACAGCGAGGC GGTGGTGGNC GTCGACGCGG	480
	TOTCCTTCAC TITOCTUCAT GATCAACTGC ANTONOTISCT GGACACGCTC TCCGAGCGTW	340 .
	AGGCGGGGGT GOTGCGGCTA COCTTCGGCC TTACCGACCG CCAGCCGCGC ACCCTTGACG	600
	AGRICOGCCA GUICTACOGC GIGRECCOGG ARCGCATOUG CCAGRICGAR ICCAAGRCIA	660
	TOTOGRASTI SCOCCATOCO AGCOSCIONO AGGICOTISCO COACTATOUT GOOGRAFICG	730
55	SCACGAGCCG TITTGAGGIG CACGCCCAGA COUTSGAGGA CGAGGCTCGC CGGATGTGGG	780
	OSTCOSOGCA AAACATTTCC SOTGCGGSCT GGACTGCCAT GGCCGANGCG ACCTCCCTAG	840
	ACRECATIGOS CONGATIGANS CAGUGUSTITO GONACATOUT GARCATIGOTO CAGUGARITAS	988
	COMMANDER CONTROL AND COMMAND AND COMMAND THE COMMAND AND COMMAND COMMAND AND COMMAND AND COMMAND AND COMMAND AND COMMAND AND COMMAND COMMAND AND COMMAND COMMAND AND COMMAND COMMAND AND COMMAND COMMAND COMMAND COMMAND COMMAND COMMAND COMMAND COMMAND COMMAND	860

GTNACROSCT SCTTCOCGAC SCCAACAACT ACGAACAGCA AGAGCASGCC TCCCAGCAGA

	TCCTCAGCAG	CTGACCCGGC	CCGACGACTC	AGGAGGACAC	ATGACCATCA	ACTATCAATT	1020
	COOCGACGTC	GACOCTCATO	GCGCCATGAT	CURCOCTCIN	COCCOCTTCC	TGOAGGCCGA	1080
	GCATCAGGCC	ATCATTTCTG	ATGTGTTGAC	CGCGAGTGAC	TTTTGGGGCG	GCGCCGGTTC	1149
	GGCGGCCTGC	CAGOGOTTCA	TTACCCAGTT	GOGCCOTAAC	TTCCAOGTCA	TOTACCACCA	1200
5	GGCCAACGCC	CACGGGCAGA	AGGTGCAGGC	TGCCGGCAAC	AACATGGCAC	AAACCGACAG	1260
	CGCCGTCGGC	TECRGCTGGG	CUTAACCCGG	OTCCTARGTY	GGGTCCGCGC	AGGGCGGGCC	1320
	GATCAGCGTC	CACTITGGCO	CCCGATACAC	GOGCATUTRG	TWOTCGGGAA	CACTRECORCE	1380
	GCGTCAGCTG	SCCGCTTCCC	CTTOTTCGGC	GACGTGCTCG	CTGATGOCTT	TURCURCUTC	1440
	1703C033G03	COGCCAATCA	ATTGGTCGCG	CHISCOTOTA	GCCTCCTGCC	GAATTCGGCA	1990
10	CGAGGGTGCT	GGTGCCGCGC	TATOSSCAGO	ACGTUAGCTC	CACGACGAAC	TCATCCCAGT	1886
	GCTGGGTTCC	CCOGACTICS	GCATCGGCGT	GTCGGCCGGA	AGGCCCATCO	COMBCCACA?	1620
	CCCCCCCAA	eccoctres	ASTACACCOT	CATCGGCGAC	COMPTCAACO	AGGCCGCCCG	1680
	GCTCACCGAA	CTGGCCAAAG	TCGLOGATGG	CCACGTTCTG	GCGTCGGCGA	TOGOGGTCAG	1740
	TGGCGCCCTG	GACGCCGAAG	CATTGTGTTG	GGATGTTGGC	GAGGTGGTTG	AGCTCCGCGG	1890
15	ACGTGCTGCA	CCURCCCAAC	TAGCCAGGCC	AATGAATNIG	GCNGCACCCG	AAGAGGTTTC	1560
	CAGCGARGTA	CGCGGCTAGT	COCOCTTOCC	**OCMPTCTTC	GOCGGCACCT	TCCGGGCXGC	1920
	TTTCCTMXCT	eccorrre	CCGGACCCCG	GGCTCGGCGA	FORGCCAACA	GCTCGGCGGC	1,980
	GOGCTCGTCG	OTTATOGAAO	CCACOTHGTC	GCCCTTACGC	AGGCTGGCAT	TGGTCTCACC	2048
	GTCGGTGACG	TACGGCCCGA	ATCGGCCGTC	CTTGATGACC	ATTGGCTTGC	CAGACGCCGG	2100
20	ATMTGMTCCC	AGCTYCGCGCA	GCGGCGGAGC	CGAAGCGCTT	TGCCGGCCAC	GACNITICGG	2150
			CTTCGTCGAG		AATATATGGT	CITCOSTGAC	3530
		GAATCOTTOC	COCCCTTTAG	ATACOCTOMS	TROCGCCCOT	MITGOGGGGT	2280
	GATNIC						2286
25	(2) INPORM	ATION FOR SI	01:0% CI Q				
		A) LENGTH:	ACTERISTICS 1136 base p polece scid				
30			NESS: sing!	l &			

- (ii) MOLECULE TYPE: DER (genomia)
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	GGGCATCTTC	CCCGACCGCG	CCTCGATCAT	CCCCCCCCC	GRAGCCGTCC	TOGOCOGRACA	60
	ACACGACGAA	TOGATOGAAG	GACGGCGCTA	CCT999GCCTC	GAGGTCCTCA	CCCGAGCCCG	126
	AGCAGCACTG	ACCAGCACCG	AAGAACOGCC	AAGCAGCAAA	CCACCBACAC	CCCAGCACTG	180
40	ACCACCTAGA	CTOCCACCO	AAGGATCAGG	CGAGGAACCT	TCACTCGTAC	ACCACGTCCC	240
	TOGCCTTGGC	CTGGTGTCAG	GCCCAGCTGG	AGCCGACGGC	GCTGTCGGTT	TGCGCCATGT	300
	TOTTOCCGGC	AGCCTGCACC	TTCTGCCCGT	GGGCGTTGGC	CTGCTCGTAG	ATCACCTOGA	360
	AGTTACGGCC	CAACTOGUTA	ATGAACCCCT	GGCAGGCCGC	CGRACCGGCG	CCGCCCCAAA	420
	AGTCACTCGC	GGTCAACACA	TCACGAATGA	TGGCCTGATG	CTCGGCCTCC	AGCAACCCGG	486
45	CCTGAGCGCG	GATCATOGCG	CCGTGAGCGT	COACATCACC	GNACTOATAG	TTGATGGTCA	540
	TOWARDOTT	TETECTTEGE	TTGTAAAAGT	ATTGTGCTGC	AGCGGCTGAC	GTTAGCTGCT	500
	CAGGATCTGC	TOGGAGGCCT	GCTCTTGCCT	CGTGCCGART	TOGGCACGAG	AGGCCGCCTT	660
	COMMINATO	CTTTGAGAAT	TCGCCAAGGC	COTCGACCCA	GCATGGGGTC	AGCTCGCCAG	720
	CCGCGCCGGC	TOGCAACOGT	TCCCGCTCQA	GAAAGACCTG	CAGGAATACC	AGTUACRAAC	780
50	GACCTOCCAG	ACGTCCGAGA	GCGTGACGGC	GGTCCACGTC	COSCTCCTCC	TOCTOGCOGG	840
	CCACGCTTGT	CAGACGTGTG	GGTTTACAAC	GGGCGGGCGT	ACGACCTGAG	TGAGTGGATT	900
	TCCAAGCATC	dcaddaddac	CITNITCATT	GGGCGGACCA	AGAACCGCGA	CATCACCGCA	560
	ATCOTCAAGT	CCTACCATES	TOATCCGGCG	ATTGTCGAGC	GAATOCTUCA	GCGGAGGTAC	1020
	GCGTTGGGCC	GCGACGCAAC	CCCTAGGGAC	ATTCCACCCCA	AGCACAATGC	ACCGCCATTT	2080
55	CTOTTCAAAG	ACGRETTERA	CAGCTGGCGG	GACACCOCGA	AGTATCGATT	MOACOA	113€

<sup>(2)</sup> INFORMATION FOR \$80 ID NO.11:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 967 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOMOGY: linear	
	(ii) MOLECULE TYPE: DEA (genomic)	
16	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
10		
	TGAGCGCGAA CCCTACCGTC GGTTCGTCAC ACGGACCGCA TGGCCTGCTC CGCGGACTGC	60
	CUCTAGOGIC GCOGATCACT COGCUTAGCO GCOCCTTTGC CCACCGATAT GGGTTCCGTC	120
	ACACTOTOCT TOCCOCCCC CCATCOCCCC GATAACGCCA TGACCTCAGC TCGGCAGAAA	289
	TEACARTECT CCCARAGECE TERGCACCOO ARGACARCER ACCAGGAGAT CECRTECCET	240
15	TYGYGACTAC CCARCCAGAA GCACTGGCGG CGGCCGG CAGTCTGCAG GGAATCGGCT	309
	COGCATTGAA COCCCAGAAT GCGGCTGCGG CGACTCCCAC GACGGGGGG GTCCCGCCGC	3.60
	CECCHATHAA MIGICOSCOC IGACONOONC TCACTICOCO OCACACOCCC AGATCIAICA	420
	GGCCGTCAGC GCCCAGGCCG CGGCGATTCA CGAGATGTTC GTCAACACTC TACAGATGRG	486
	CICAGGGTGG TATGCTGCTA CCGAGGCCGC CAACGCGGCC GCGGCCGGRT AGAGGAGTCA	540
20	CTUCCATGA TITTEGGGCG TTUCCGCCGG AGGICAATTC GCTGCGGATG TATGCCGTTC	600
	CTOSCTOGGC ACGATUSTO DOTGCOGCT CODCCTOGAL COGCTOGGC GCGGAGCGA	660
	STICGGCCOC CACCOSTIAT GAGACGCTGA TCACTCASCT CAGCAGTGAG GGGTGGCTAG	720
	STOCKSCOTC ACCOCCATE SCCSAGGCAG TTSCSCCGTA TSTSGCGTGG ATGASTGCCG	786
	CTGCHGCBCA AGCCGAGCAG GCGGCCACAC AGGCCAGGGC CGCCGCGGCC GCTTTTUAGG	840
25	GGGGGTTTGC CGCGACGGTG CCTCCGCCGT TGATCGCGGC CAACCGGGCT TCGTTGATGC	900
	AGCTGATCTC GACGAATGTC TTTGGTCAGA ACACCTCGGC GATCGCGGCC GCCGAAGCTC	989
	AGTACOC	967
	(2) INFORMATION FOR SEC ID NO:12:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LEMNYE: SES base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: Single	
35	(5) TOPOLOGY: linear	
	(5: 10-03001) 224001	
	(15) MOLECULE TYPE: DNR (genomic)	
	,	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
40		
	TGGATTCCGA TAGCGGTTTC GGCCCCTCGA CGGGCGACCA CGGCGGGGGAG GCCTCCGAAC	80
	OGGOGGCUNG GAUGUTGOGA TYCGUCGGGA CUGCAAUCAA AGAACGCUNG GYUUGUGUGU	120
	TOGGGCTGRC COURCTGGCC GGTGRTGRGT TOGGCRACGG CCCCCGGRTG CCGRYSGTGC	1.80
	COGGGACCTG GGAGCAGGGC AGCAACGAGC CCGAGGGGCC CGACGGATCG GGCAGAGGGG	240
45		300
. 70.0	OGGTOBAAAG GAGAGATGIT ATGAGCCTTI TXGATGCTCA TRICCCACAG TIGGTGGCCT	360
	COCAGTOGGO GITTECOGGO AAGGOGGGGO TGATGOGGCA CACGATGGGI CAGGGGGAGC	420
	AGGCSGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG	400
	COCATGOCOG STITTSTOGOG GOGGOCGOCA AASTGAAGAC CTTGITTSGAT GICGOGGAGG	840
50	CGAATCROGG TGAGGCCGCC GOTACCTAYG TGGCCGCCGA TGCTG	585
30	COMMING ADMONICACE MATHEMATICA ADMINISTRA ARCAG	3.00
	(2) INFORMATION FOR SEQ ID NO:13:	
00	(i) SECONNUL CHARACTERISTICS:	
55	(A) LEWGTE: 144 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	

- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: \$80 ID NO:13:
- 5 Als Leu Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Ala 1.0 Lou Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val
- 25 10 Met Ber His Tyr Gin Ala Val Ala His Glu Ile Trp Cys Leu His Glu 40 45
  - Mas Ala Ser Ser Gly Lys Pro Trp Ala Ser Ile Thr Thr Gly Ala Pro 5.5 60
- Gly Ser Pro Ala Ser Thr Thr Arg Ser Arg Thr Pro Leu Val Ser Thr 15 70 75 Asn Arg Xea Val Xsa Ala Pro Tle Val Ser Pro Asn His Thr Gly His 85 90
- Arg Pro Glu Lys Gly Leu Gly Ser Xaa Gin Arg Arg Leu Ser Arg Val 200 105 20 Leu Pro Arg Ile Ile Amp Arg Pro Ala Cly Pro Xee Cly Pro Pro Leu
  - 320 325 The Ser Gly Ser His Phe Leu Cys Ser Trp Ris Gly Tyr Ser Ser Gla 135 140
  - 25 (2) INPORMATION FOR SEC ID NG:14:
    - (f) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 382 amine acids
  - (B) TYPE: amino acid 30 (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: peoride
  - 35 (xi) SBOURNCE DESCRIPTION: SEO ID NO:14:

100

- His Ala Leu Ala Ala Gin Tyr Thr Glu Ile Ala Thr Glu Leu Ala Ser 3.0 3.5 Val Leu Ala Ala Val Gin Ala Ser Ser Trp Gin Gly Pro Ser Ala Asp
- 40 20 25 Arg Phe Vel Val Ala His Gln Pro Phe Arg Tyr Trp Leu Thr His Ala 35 40 Ala Thr Val Ala Thr Ala Ala Ala Ala Ala His Xsa Thr Ala Ala Ala
- 45 Cly Tyr Thr Sor Ala Leu Cly Cly Met Pro Thr Leu Ala Glu Len Ala 75
- Ala Asn His Ala Met His Gly Ala Leu Val Thr Thr Asn Phe Fhe Gly 85 90 Val Asm Thr Ile Pro Ile Ala Leu Asm Glu Ala Asp Tyr Leu Arg Met 50
- Trp Ile Gln Ala Ala Thr Val Met Ser His Tyr Gln Ala Val Ala His 120 Giu Ser Val Ala Ala Thr Pro Ser Thr Pro Pro Ala Pro Gln Ile Val
- 135 140 55 Thr Ser Ala Ala Ser Ser Ala Ala Ser Ser Ser Phe Pro Asp Pro Thr 150 155
- Lys Leu Ile Leu Gin Leu Leu Lys Asp Phe Leu Giu Leu Leu Arg Tyr 165 170

105

	Leu	Ala	Val	Glu 180	Leu	iou	Pro	Gly	Pro 185	Letu	Gly	Asp	Leu	11e	Ala	Gln	
	Val	Lew	Asp 195	Tro	Phe	lie	Ser	Phe 250		Ser	gly	Pro	Val. 205		Thx	She	
5	Leu	Ala 210		Leu	Val	Leu	Asp 235		Leu	Ile	Tyr	Phe 220		Sco	Phe	Ala	
	Pro 225		Thr	Ser	Pro	Val 230		Leu	Pro	Ala	Val. 235		Less	Arg	Asn	Arg 240	
10		Lys	Thr	Ala	Thr 245	Gly	Leu	TIX.	Leu	Pro 250	Pro	Thr	Val	lle	Phe 255	Asp	
	His	Pro	Thr	Pro 260	Thr	Ala	Val	Ala	01u 265	Tyr	Val.	Ala	Gla	01n 270	Met	Sex	
	Gly	Ser	Arg 275	Pro	Thr	Glu	Sex	Gly 280	Asp	Pro	The	Sex	Gln 285	Val	Val	Glu	
15	Pro	Ala 290	Arg	Ala	Glu	Phe	Gly 295	Thx	Ser	Ala	Val.	His 390	Gln	He	Pro	Pro	
	Apg 305	Pro	Alm	Asp	The	Arg 310	Arg	Ala	Сув	Arg	His 315		Asp	Asp	Asy	Pro 320	
20		Asp	Ser	Arg	11e		Gin	His	Arg	Asp 330		Ala	Oly	Leu	Asp	Pro	
	The	Glu	Arg	G1y			ឲារប	Gly	Asp 345			Leu	Val	Ser 350	Gly	Trp	

(2) INFORMATION FOR SEC ID NO:18: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 amino acids 5 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MCLECULE TYPE: peptide 10 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:15: Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr 10 15 Ala Val Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn 30 25 30 Bly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val 35 60 45 The Thr Gin Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala 20 Met Ala Giu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala 70 75 Ale Gln Ala Glu Gln Ala Ale Thr Gln Ala Arg Ala Ala Ala Ala Ala 85 90 25 Fire Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala 305 210 3.00 Asn Arg Ala Ser Leo Met Gln Leu Ile Ser Thr Asn Val Phs Gly Gln 120 325 Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gin Tyr Gly 30 130 135 (2) INFORMATION FOR SEQ ID NO:15: (i) SEQUENCE CHARACTERISTICS: 35 (A) LENGTH: 58 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) ToPoLogy: linear 40 (ii) WOLECULE TYPE: pentide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: Met Ala Ser Arg Phe Met Thr Asp Pro Ris Ala Met Arg Asp Met Ala 45 213 Oly Arg Phe Glu Val Sis Ala Gin Thr Val Glu Asp Glu Als Arg Arg 26 28 30 Met Trp Ala Ser Ala Gin Asn Ile Ser Gly Ala Gly Trp Ser Gly Met 35 80 50 Ala Glu Ala Thr Ser Leu Asp Thr Met Thr 30 (2) INFORMATION FOR SEC ID NO:17: 55 (i) SECURECE CHARACTERISTICS:

(A) LENGTH: 67 amino scids (B) TYPE: amino acid (C) STRANDRONESS: singl\*

## (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
- 5 Mat Thr Ile Aso Tyr Cln Phe Gly Asp Val Asp Ala His Gly Ala Met 15 The Arg Ala Gin Ala Ala Ser Leu Glu Ala Glu His Gin Ala Ile Val 20 25
- 10 Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Sly Ala Gly Ser Val 35 40 Ala Cys Win Glu Phe lie Thr Gin Leu Gly Arg Asn Phe Gin Val Ile 55 60 50 Tyr Glu Gla 15 85
- (2) INFORMATION FOR SEC ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: pectide

20

- (xi) SEQUENCE DESCRIPTION: SEO ID NO:18:
- Met Ala Ser Arg Phe Net Thr Asp Pro Bis Ala Met Arg Asp Net Ala 30 10 Gly Arg Phe Glu Val Bis Als Gln Thr Val Glu Asp Gln Ala Arg Arg 25
- Met Trp Ala Ser Als Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met 3.5 40 45 35 Ala Glu Ala Thr Ser Leu Asp Thr Met Thr 55
- (2) INFORMATION FOR SEC ID NO.19:

58

- 40 (i) SECUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- 45
  - (ii) NOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
- 50 Met Thr Ile Asn Tyr Gin Phe Gly Asp Val Asp Ala His Gly Ala Met 3.0 The Arg Ala Gin Ala Ala Ser Leu Glu Ala Giu His Gin Ala Ile Val 35
- 55 40 Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gin Val Ile

Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val

70 68 75 8.0 Ass Met Ala Gin Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 85 5 (2) IMPORMATION FOR SEQ ID NO:20: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 amino acids (B) TYPE: amino acid 16 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20: Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn 3.0 Tyr Gla Gla Gla Gla Gla Ala Ser Gla Gla Ile Leu Ser Ser 26 20 (2) INFORMATION FOR SMG TO NO:21: (i) SHOURNCH CHARACTERISTICS: 25 (A) LEMGTH: 94 amino acids (B) TYPE: amino soid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: peptide (xi) SECURNCE DESCRIPTION: SEC ID NO.21: Met Thr lie Asn Tyr Gin Phe Gly Asp Val Asp Ala Mis Gly Ala Met 35 30 Ile Arg Ala Gin Ala Gly Leo Leo Glu Ala Glo His Gha Ala Ile Ile 24 Arg Asp Vel Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala 35 40 40 Ala Cys Gin Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gin Val Ile 58 Tyr Gla Gin Ala Asn Ala Ris Gly Gln Lys Val Gin Ala Ala Gly Asn 70 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 45 RK (2) INFORMATION FOR SBO ID NO:22: (i) SECUENCE CHARACTERISTICS: 50 (A) LENGTH: 69 amino acids (B) TYPE: amino acid (C) STWANDEDNESS: single (D) TOPOLOGY: linear 33 (ii) NOLECULE TYPE: paptide (xi) SECUENCE DESCRIPTION: SEC ID NO:22:

Ala Arg Arg Not Trp Ala Ser Ala Gin Asn Lie Ser Gly Ala Gly Trp 3.6 Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Glu Met Asn 20 25 Gin Ala Phe Arg Asm Ile Val Asm Met Leu His Gly Val Arg Asp Gly 4.0 4.5 Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln

55

Gln ile Leu Ser Ser

10 65

5

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- (2) INPORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS: (A) LEWOTH: 54 amino acids
  - (D) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- 20 (15; MOLECULE TYPE: peptide
  - (xi) SECUENCE DESCRIPTION: SEC TO NO:23:
- Met Thr Ile Asn Tyr Glo Phe Gly Asp Val Asp Ala Bis Gly Ala Net 25 The Arg Ala Gin Ala Gly Lou Lou Glu Ala Gin His Gin Ala The Ile 28 Arg Asp Val Deu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala

3.5 45 30 Als Cys Gin Gly Phe Ile Thr Gin Lea Sly Arg Asn Phe Gin Val Ile 30 44

- Tyr Glu Gln Ala Aen Thr His Gly Gln Lys Val Gln Ala Ala Gly Aan 7.0 75 Asn Met Ala Gln Thr Asp Ser Ala Val Xaa Ser Ser Trp Ala 35 935 90
- (a) IMPORMATION FOR SEQ ID NO:24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENCTH: 52 amino acids (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPGLOGY: linear
- 45 (ii) NOLECULE TYPE: peptide
  - (xi) SECURNCE DESCRIPTION: SEC ID NO:24:
  - Gly Met Ala Slu Ala Thr Ser Xaa Asp Thr Met Thr Gin Met Ash Glo 50 10 Ala Phe Arg Asn Ile Val Asn Met Leu Sis Gly Val Arg Asp Gly Leu 25 Val Arg Asp Ala Asp Kaa Tvr Glu Gln Gln Glu Gin Ala Ser Gln Gls 40
  - 35
- 55 Ils Leu Ser Ser 50
  - (2) INFORMATION FOR SEC ID NO: 25:

	(1)		LES	MG118	94	ans.	no a									
5		10	ST	PE: 4 RANDI POLO	RONK	88:	sing	i.e								
	(11)	MOL	SCUL	E TY	92: 1	pept	ide									
10	(xi)	SBQ	78NC	E DE	ecrz	P770	N: 3	8Q I	081 (0	:25:						
	Met	Thr	Tle	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	Mis	Gly	Ala 15	Mer
15	fle	Arg	Ala	Gln 20	Ala	Gly	Ser	Leu	01ts 25	Ala	Glu	His	din	Ala 30	Ile	Ile
	Ger	App	Val 35		Thr	Ala	Ser	Ang.		Trp	eta	Gly	Ala		Ser	Ala
	Ala	Cys 50	Gln	Gly	Phe	rie	Thr		Leu	Gly	Arg	Asn 60		Oln	Val	Xas
20	Tyr	G.I.u	ola	Ala	Asn	Ala 70	His	Gly	Gla	Lyn	Val 75	Oln	Ala	Ala	siy	Asn 80
		Met	Ala	Gln	Thr 85		Ser	Ala	Val	Gly 90	Ser	Ser	Trp	Ala		
25 (2)	INFO	emat:	EON I	POR :	SEQ.	n s	0:26	2								
30	(1)	18	AA.	E CH NGTS PO: RANC: POLO	: 98 amin BONE	ami o ac ss:	no a id aing	oids								
	(11)	MOL	BCUL	e TY	PR	pept	ide									
35	(xi)	BBQ	JERC.	e de	SCRI:	Prio	8 : S.	BQ I	9 NO	:26:						
	Met 1	Thr	Ser	Arg	Phe 5	Net	Thr	Asp	Pro	His 20	Ala	Met	Arg	Asp	Met 15	Als
40	Gly	Arg	Fhe	20	Val	His	Ala	Gln	Thr 28	Val.	Olu	Asp	Giu	Ala 30	Arg	Arg
	Met	Trp	Ala 35	Ser	Ala	gin	Asn	Tle	Ser	GIY	Ala	Gly	Trp	Ser	GJA	Me S
	Ala	Glu 50	Ala	Thr	Ser	Leu	889 55	Thr	Met	Ala	Gla	Met 60	Asn	Gln	Ala	Phe
45	65	.Asn				70					75					80
		Ala	Asn.	Asn	Tyr 85	Glu	Gln	Gln	Glu	Gln 90	A) a	Ser	Gìn	Gln	Tle	Leu
50	Ser	ser														

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids
  - (B) TYPE: amine sold (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (Li) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
- 5 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 1 5 10 15 Fle Arg Ala Xaa Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
- 20 25 30 Ser Asp Val Lou Thr Ale Ser Asp Phe Trp Gly Gly Ale Gly Ser Ale 10 35 45
  - Als Cys Gin Gly Phe Ile Thr Gin Leu Gly Arg Asn Phe Gin Val Ile 50 55 56 56 Tyr Glu Gin Als Asn Ale His Gly Gin Lys Val Gin Als Als Gly Asn
- - (2) INPORMATION FOR SEC ID NO:28:
  - 20 (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 amino acide (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
- 30 Arg Phe Glu Val His Ala Oln Thr Val Qlu Asp Oln Ala Arg Arg Met 1 5 10 15 Trp Ala Ser Ala Oln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala
- Xaa Ala Thr Ser Leu Asp Thr Met Ala Gla Met Asn Gla Ala Phe Arg
  35 46 45
  Ann fle Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp
  50 60
- Als Asn Asn Tyr Gin Gin Gin Glu Gin Als Ser Gin Gin Ile Leb Ser  $65 \\ 70 \\ 75 \\ 86$ 
  - (3) INFORMATION FOR SEQ 10 NO:29:
- (i) SEQUENCE CHARACTERISTICS: 45 (A) LEMBTE: 94 amino acide
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

38 40 45 Ala Cys Gin Gly Pac Tie Thr Gin beg Gly Arg Asa Phe Gin Val Ile 35 83 Tyr Glu Glu Ala Asn Ala Mia Gly Glu Lys Val Glu Ala Ala Gly Asn 5 20 78 Asn Met Ala Gin Tor Asp Ser Ala Val Gly Ser Ser Trp Ala 8.5 90 (2) INFORMATION FOR SEG ID NO:30: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDSDESSS: single 15 (B) YOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID No:30: 20 Gln Glu Gla Ala Ser Gln Gin Ile Leu Ser Ser (3) INFORMATION FOR SEC ID MC:31: 25 (1) SECRENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (S) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 30 (ii) MCLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEC ID NO:31: 35 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 10 3.5 The Arg Ala Gin Ala Gly bou bou Gin Ala Giu Mis Gin Ala The The 20 25 Arg Asp Val Leu Thr Ale Ser Asp Phe Trp Gly Gly Ale Gly Ser Ale 40 35 Als Cys Gin Gly Phe Ile Thr Gin Leu Gly Arg Asn Phe Gin Val Ile Tyr Glu Gin Ale Asn Ale His Gly Gin Lys Val Gin Ale Ale Gly Asn 70 75 45 Asn Net Ala Sin Thr Asp Ser Ala Val Cly Ser Ser Trp Ala 25 90 (2) INPORMATION FOR 980 ID NO:32: 50 (i) SEQUENCE CHARACTERISTICS: (A) LEMSTH: 99 amino soids (B) TYPE: amino acid (C) STRAMDEDNESS: single (D) TOPOLOGY: linear (ii) NOLECULE TYPE: poptide

(xi) SEQUENCE DESCRIPTION: SEG ID NO:32:

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala 10 Asn Leu Gin Gly Ile Gly Thr Thr Net Asn Ala Gin Asn Ala Ala Ala 5 20 28 Als Als Pro Thr Thr Gly Val Val Pro Als Als Als Asp Glo Val Ser 40 Ala Leu Thr Ala Ala Gim Phe Ala Ala Bis Ala Gim Wet Tyr Gim Thr 88 60 10 Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn The Lev 35 77.00 Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala 88 90 95 Ala Ala Gly 15

- (2) IMPORMATION FOR SHO ID BO:33:
  - (i) sequence characteristics:
    - (A) LENGTH: 99 amino acids
    - (S) TYPS: amino acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: peptide

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

35 Als heu Thr Als Als Gln Phe Als Als Sis Als Gln Met Tyr Gln Th

Ala Leu Thr Ala Ala Gla Phe Ala Ala His Ala Gla Met Tyr Gln Thr 50 Val Ser Ala Gla Ala Ala Ala Ile His Slu Met Phe Val Asc Thr Leu 85

Val Ala Ser Eer Oly Ser Tyr Ala Ala Thr Olu Ala Ala Asa Ala Ala Ala
40
Ala Ala Giy

- (2) INFORMATION FOR SEQ ID NO:34:
- 45 (i) SEQUENCE CHARACTERISTICS:

  (A) LENGTH: 15 amino acids

  (B) TYPE: amino acid
  - (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
  - ----
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
- 55 Amp Pro His Ala Met Arg Amp Met Ala Gly Amg Phe Glu Val His 1 5 10 15
  - (2) INFORMATION FOR SEQ ID NO:25:

(i) SECRIENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino sold 5 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 0 (xi) SEQUENCE DESCRIPTION: SEQ ID 80:35: Ary Amp Met Ale Gly Arg Phe Glo Val Bis Ale Glo Thr Val Glo 3.6 (2) INFORMATION FOR SEC ID NO.36: (I) SECURNCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid 0 (C) STRANDEONESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Als Arg Arg 5 10 0 (2) INFORMATION FOR SEQ ID BO:37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino soid 5 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 0 (xi) SECURNCE DESCRIPTION: SEC ID NO:37: Ala Gln Thr Val Glu Asp Glu Ala Arg Arg Net Trp Ala Ser Ala 10 (2) IMPORMATION FOR SEQ ID NO:38: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid 0 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peotide 5 (xi) SECTENCE DESCRIPTION: SEC 10 NO.38: Asp Glu Ala Arg Arg Net Trp Ala Ser Ala Glo Ass lie Ser Gly 10 15

(2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: 5 (A) LENGTH: 15 amino acids (B) TYPE: smine acid (C) STRANDEDNESS: mingle (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: peptide (xi) SBOUENCE DESCRIPTION: SEC ID NO:39: Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Als Gly Trp Ser Gly 15 10 (2) INPORMATION FOR SEQ ID NO:40: (1) SEQUENCE CHARACTERISTICS: 20 (A) LENGTH: 16 amino acide (B) TYPE: amino acid (C) STRANDEDNESS; single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: 880 TD NO:40: Gin Asn Ile Ser Sly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr 30 8 15 10 (2) INPORMATION FOR SEC ID NO: 41: (1) SECUENCE CHARACTERISTICS: 35 (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 40 (ii) MOLECULE TYPE: peptide (ki) SEQUENCE DESCRIPTION: SEQ ID NO:43: Ala Gly Trp Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Thr 45 10 (2) INFORMATION FOR SEC ID NO:42: (i) SEQUENCE CHARACTERISTICS: 50 (A) LENGTH: 15 amino scids (B) TYPE: amino acid (C) STRANDERWESS; single (b) TOPOLOGY: linear 55 (\$1) MOLECULE TYPE: peotide (x1) SECURNCE DESCRIPTION: SEC ID NO:42:

Met Ala Glu Aia Thr Ser Lou Asp Thr Met Ala Gin Met Asn Gin 10 (2) INFORMATION FOR SEQ ID NO:43: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amine acids (B) TYPE: amino soid (C) STRANDEDNESS: single 16 (D) TOPOLOGY: linear (ii) MOLECTLE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: 13 Ser Neu Asp Thr Met Ala Gin Mat Ash Gin Ala Phe Arg Ash Tie 10 (2) INFORMATION FOR SEC ID NO:44: 20 (i) SECUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: pentide (xi) SECURNCE DESCRIPTION: SEC TO NO:44: 30 Ala Gln Met Asn Gln Ala Phe Arg Asn lie Val Asn Met Leu His 5 20 (2) INFORMATION FOR SEQ ID NO:45: 35 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: smine seid (C) STRANDEDNESS: single 40 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEG ID NO:45: 45 Ala Pae Arg Asn lie Val Asn Met Leu His Sly Val Arg Asp Sly 1.0 (2) INFORMATION FOR SEQ ID NO:46: 50 (i) SHOURNCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDMESS; single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(xi) SECURACE DESCRIPTION: SEC ID NO:46: Val Asm Met Leu His Oly Val Arg Asp Cly Seb Val Arg Asp Ala 8 20 4 (2) INFORMATION FOR SEC ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 10 (B) TYPE: amimo acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SECURNCE DESCRIPTION: SEC ID NO.47: Sly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln 10 20 (2) INFORMATION FOR SEQ ID NO:48: (i) SECUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 25 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: Linear (ii) MOLECULE TYPE: peptide 30 (xi) SECUENCE DESCRIPTION: SEC ID NO:48: Leu Val Arg Asp Als Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser 5 10 35 (2) IMPOSMATION FOR SEQ ID NO:49: (i) SECUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids 40 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (il) MOLECULE TYPE: peptide 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49: Asn Asn Tyr Glu Gin Glu Glu Glu Ala Ser Gln Gin Ile Leu Ser Ser 3.0 5 1.5 50 (2) INFORMATION FOR SNQ ID NO:50: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids 55 (8) TYPE: amino soid (C) STRANDEDNESS: single (D) TOPCLOGY: linear

- (ii) MOLECULE TYPE: pepcide
- (xi) SECURNCE DESCRIPTION: SEQ ID NO:50:
- 3 Met Ala Ser Arg Phe Met Thr Asp Pro Ris Ala Met Arg Asp Met Ala 5 1.0 dly
- (2) INFORMATION FOR SEQ ID NO:51:
- 10 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino scids (B) TYPS: amino scid
- (C) STRANDRONESS: single 15 (D) TOPOLOGY: linear

  - (41) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: GEQ ID NO:51: 20

Met Thr lle Asn Tyr Glm Phe Gly Asp Val Asp Ala His Gly Ala 10

- (2) INFORMATION FOR SEC ID NO:52: 25
- (i) SECURNCE CHARACTERISTICS:
  - (A) LENGTE: 15 smine acids
    - (B) TYPE: smime acid
- (C) STRANDEDNESS: single 30 (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
- 35 Gls Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Glo 15
- (2) INFORMATION FOR SEC ID NO.53: 48
  - (1) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acide

(will showener procription: sho in mo:sa:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

- (B) TYPE: amino acid
- (C) STRAMBEDMESS: single (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: peptide

45

- 50 Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu 3. 8 3.0
  - (2) INFORMATION FOR SEC ID NO: 54:
  - (i) SECURICE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acida
    - (B) TYPE: amino acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide ŝ (x1) SECTIONCE DESCRIPTION: SEC ID NO:54: Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu Bis Gln Ala 3.0 30 (2) INFORMATION FOR SEQ ID NO:55: (i) SBOUSNCE CHARACTERISTICS: (A) LENGTH: 15 amian solds 15 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLDCULE TYPE: peptide 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: Als Als Ser Leu Glu Ala Glu Ris Gln Ala Ile Val Arg Asp Val 5 25 (2) INFORMATION FOR SEC ID NO:56: (i) SECURNCE CHARACTERISTICS: (A) LENGTH: 15 amino scide 30 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: Linear (ii) MOLECULE TYPE: peptide 35 (xi) SEGUENCE DESCRIPTION: SEG ID NO:56: Ala Glu Mis Gln Als Ile Val Arg Asp Val Len Ala Ala Gly Asp 10 40 (2) INFORMATION FOR SEC ID NO:57: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 45 (B) TYPE: emine soid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 56 (xi) sequence description: seq id No:57: Tie Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala 5 3.0 55 (2) IMPORRATION FOR SEC ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) DENGTH: 16 amino acids

(8) TYPE: amino acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

16 two Ala Ala Sly Asp Phe Trp Sly Sly Ala Sly Ser Val Ala Cys Gln 1.0

(2) IMPORMATION FOR SHO ID NO:59:

(i) SECUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids (B) TYPE: amino acid

(C) STRANDEDWESS: single

(D) TOPOLOGY: linear

26 (ii) MOLECULE TYPE: peptide

(xi) SECURNCE DESCRIPTION: SEC ID NO:55:

25 Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe lie Thr 5 1.0

(2) INFORMATION FOR SEG ID NO: 60;

30 (i) SEQUENCE CHARACTERISTICS: (A) LEMGTH: 15 amino acids

35

40

50

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) NOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn 3.0

(2) INFORMATION FOR SEQ ID NO:61:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

55 Gin Glu Phe fle Thr Gin Leu Gly Arg Asn Phe Cin Val fle Tyr Glu 1.6 3.5 Glo Ala

(2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 5 (8) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: Arg Asn Phe Gin Val The Tyr Glu Cln Ala Asn Ala His Gly Sla 5 10 15 (2) INFORMATION FOR SEQ ID NO:63: (1) SECURNCE CHARACTERISTICS: (A) LENGTH: 15 amino scide 20 (E) TYPE: amino acid (C) STRANDEDNRSS: single (D) TOPOLOGY: linear ((i) MOLECULE TYPE: peptide 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.63: The Tyr Glu Gln Als Asn Ala His Gly Gln bys Val Gla Ala Ala 3.0 30 (2) INFORMATION FOR SEC ID NO:64: (i) SECUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 35 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64: Asn Ala Bis Cly Cln Lys Val Cln Ala Ala Oly Asn Asn Met Ala 2 10 44 (2) INFORMATION FOR SEQ ID NO:65: (i) sequence characteristics: (A) DEMGTH: 15 amine acids 50 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 55 (xi) SEQUENCE DESCRIPTION: SEG ID NO:65: Lys Val Gin Ale Ale Gly Asn Asn Met Ale Gin Thr Asp Ser Ala

10 15 3 (2) INFORMATION FOR SEC ID NO:66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino soid (C) STRANDEDMESS: single (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: peptide (xi) SHOURNCE DESCRIPTION: SEQ ID NO.66: Gly Asn Asn Met Ala Glo Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 15 15 (2) INFORMATION FOR SEC ID NO:67: 20 (5) SEQUEECE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 25 (ii) NOT BOUNE TYPE: peptide (will secuence description: sec 10 NO:67: 30 Asp Ala His Gly Als Met Ile Arg Ala Leu Ala Gly Leu Leu Glu 10 (2) INFORMATION FOR SHO ID NO: 68: 35 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 40 (11) MOLECULE TYPE: peptide (xi) SECUENCE DESCRIPTION: SEC ID NO:68: Asp als Ris Cly Ala Met Ile Arg Ala Cln Ala Gly Lee Leu Glu 45 8 1 (2) INFORMATION FOR SEQ ID NO: 89: 50 (i) SECUENCE CHARACTERISTICS: (A) LENGTH: 25 smine acids (B) TYPE: amino acid (C) STRANDEDW868: single (b) TOPOLOGY: linear 55 (ii) MOLECULE TYPE: peptide (xi) SECUENCE DESCRIPTION: SEQ ID NO: 69:

Met Ile Ary Ala Lew Ala Gly Leu Leu Glu Ala Glu Wis Gln Ala 3.0 (2) INFORMATION FOR SEQ ID NO:70: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino scid 10 (C) STRANDEDNESS: single (D) TOPOLOGY: Linear (ii) MCLECULE TYPE: peptide 15 (xi) SECURNCE DESCRIPTION: SEC ID NO:70: Met lie Arg Ala Gin Ala Gly Leu Leu Glu Ala Glu His Gin Ala 63 3.0 20 (2) IMPORMATION FOR SEC ID NO:71: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amisc acid 25 (C) STRANDEDNESS; single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: Ala Siv Leu Leu Giu Ala Giu Ris Gla Ala Ile Lie Ser Asp Val 3.6 35 (2) IMPORMATION FOR SEC ID NO:72: (i) SEQUENCE CHAPACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino scid 40 (C) STRANDEDNESS: single {D} TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72: Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Arg Asp Val 1 8 10 50 (2) INFORMATION FOR SEC ID NO:73: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: umino acid 55 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: pepride

(xi) EROCENCE DESCRIPTION: SEC ID NG:73: Ala Giu His Gin Ala Tie Ile Ser Asp Val Leu Thr Ala Ser Asp ŝ 1.0 (2) INFORMATION FOR SEQ 3D NO:74: (i) SEQUENCE CHARACTERISTICS: 10 (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (il) NOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74: Als Clu His Cln Ala Ilo Ilo Arq Asp Val Leu Thr Als Ser Asp 20 3 (2) INFORMATION FOR 880 ID NO:75: (i) SEQUENCE CHARACTERISTICS: 25 (A) LENGTH: 15 amino acids (B) TYPE: smine soid (C) STRANDEDNESS: single (D) TOPOLOGY: limear 30 (ii) MOLECULE TYPE: neptide (xi) EBOURNCE DESCRIPTION: SRC ID NO.75: Ile Ile Ser Asp Val Lew Thr Ale Ser Asp Phe Trp Gly Gly Ala 35 10 (2) INFORMATION FOR SEQ ID NO:74: (1) SEQUENCE CHARACTERISTICS: 40 (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDWESS: single (D) TOPCLOGY: linear 35 (ii) MOLECULE TYPE: peptide (xi) SECUENCE DESCRIPTION: SEC ID NO:76: Ile Ile Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala 50 89 10 (2) INFORMATION FOR SEQ ID NO:77: (1) SECUENCE CHARACTERISTICS: (A) LENGTH: 15 smino acids (8) TYPE: amino acid (C) STRAMDEDWESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEO ID NO.77: Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln 3.0 (3) INFORMATION FOR SEQ ID NO:78: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (S) TYPE: amdrac acid (C) STRANDEDNESS: single 15 (D) TOPCLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: 20 Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr 5 (3) INFORMATION FOR SEG ID NO:79: 25 (1) SHOURNCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 30 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SECURNCE DESCRIPTION: SEC ID NO:79: 35 Gly Ser Ala Ala Cya Gln Gly Phe Ile Thr Glo Leu Gly Arg Asn 3.0 (2) INFORMATION FOR SEC TO NO:86: 40 (i) SECURNCE CHARACTERISTICS: (A) LEWITH: 15 amino acids (8) TYPS: amino acid (C) STRANDEDNESS: single 45 (D) TOPOLOGY: linear (ii) MOUSCULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEO ID NO:80: 50 Gin Gly Phe lie Thr Gin Seu Gly Arg Asn Phe Gin Val Tie Tyr 45 25 (2) INFORMATION FOR SEQ ID NO:81: 55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 smino acids (B) TYPE: amino acid

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(C) STRANDEDNESS: single
                  (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: poptide
   5
            (x1) SECRIENCE DESCRIPTION: SEC ID NO:81:
            Val Thy Thr Asn Phe Phe Sly Val Asn Thr Ils Pro Ile Ala Leu Asn
                                                 30
  10
            Glu Ala Asp Tyr Leu Arg Met Trp Ile
                         20
       (2) INFORMATION FOR SEC 1D NO:82:
  15
           (i) SHOURNCE CHARACTERISTICS:
                  (A) LENGTH: 25 amino scids
                  (B) TYPE: amino acid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
20
          (ii) MOLECULE TYPE: peptide
            (xi) SECURNCE DESCRIPTION: SEC ID NO:82:
  25
            Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gls Ala Ala Thr Val Met
            Ser His Tyr Glm Ala Val Ala His Glu
                        20
  30 (2) IMPORMATION FOR SEQ ID NO.83:
               (i) SECURNCE CHARACTERISTICS:
                (A) LENGTH: 967 base pairs
                (B) TYPE; nucleic acid
  35
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: cDNA
  40
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
        TERREGOCCAR COCTACCETT GOTTOSTCAC ACRERCOSCA TERRECOTOCTO CECEGOROTEC
        CGCTAGGGTC GCGGATCACT CEGCCTAGCG GCCCCTTTGC CCACCGATAT GGGTTCCGTC
                                                                                120
        ACAGNITOGT TGCCCGCCCG CCATCCGCCCG GATAACGCCCA TGACCTCAGC TCGGCAGAAA
                                                                                 180
  45
        TGACARTGCT CCCAAAGGCG TGAGCACCCG AAGACAAUTA AGCAGGAGAT CGCATGCCTT
                                                                                248
        TTGTGACTAC CCAACCAGAA GCACTGGGGG CGGCGGCCGG CAGTCTGCAG GGAATCGGCT
                                                                                200
        COGCATTGAA COCCCAGAAT GOGGCTGCGG CSACTCCCAC GACGGGGGTC GTCCGGCGGC
                                                                                360
        CUCCUATUAA NTGTCGUCUC TUACOOOGC TCAUTTCCCU QCACACOCCC AGATCTATCA
                                                                                420
        SUCCOTCAGO GCCCAGGOCG CUGCGATTUA CGAGATUTTC GTCAACACTC TACAGATGAG · 480
  50
       CTCAGGGTOG TATGCTGCTA CCGAGGCCGC CAACGCGGCC GCGCCGGNT AGAGGAGTCA
                                                                                540
        CTGCGATGGA TTTTGCGGCG TTGCGGCCGG AGGICAATTC GGTGCGGATG TATGCCGTTC
                                                                                600
        CTESCICOGO ACCAATOSTO SCISCOSCOT COSCCISSAA COSOTISSOO SCEGASCISA
                                                                                660
       OTTOGGGGC CACCOGTTAT CAGACOGTGA TCACTCAGCT CAGCAGTGAG GGGTGGCTAG
        OTCCGGCGTC AGCGGCGATG GCCGAGGCAG TTGCGCCGTA TGTGGCGTGG ATGAGTGGC
      CTGCGGGGCA AGCCGAGCAG GCGGCCACAC AGCCCAGGGC CGCCCGGGCC GCTTTGAGG
CGGCGTTTGC CGCGACGGTG CCTCCGCCGT TGATCGCGGC CXACCGGGCT TGGTTGATGC
        COCCETTIC COCCACGGE CUTCOCCCT TOATCCCGC CACCGGGCT TOATCATCC 900
ASCUTATUTC CACCAATGTC TITGOTCAGA ACACCTCGGC GAUCGGGGCC GCCGAAGCTC 960
        AGTACGG
                                                                                967
```

	(3) INFORMATION FOR SEQ ID NO:84:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LEMOTH: 15 amino acids (E) TYPE; amino acid (C) STRADDENNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECTER TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
15	Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala 13 $$ 19 $$ 15	
	(2) INFORMATION FOR SEQ ID NO:85:	
29	(i) SEQUENCE CHARACTERISTICS; iA) LENGTH: 15 unimo moids (B) TYPE: amino moid (C) STRANDERMESS: single (D) TOPOLOGY (linear	
25	(11) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
	Thr Gin Pro Gis Ais Leu Ais Als Ais Ais Ass Leu Gin Gly	
30	1 5 10 15	
	(2) IMPORMATION FOR SEQ IS NO:86:	
35	(i) STQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino anids (B) TYPE; amino acid (C) STRANDEDWSSS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: poptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
	Lou Ala Ala Ala Ala Ala Asn Lou Gln Gly Ile Gly Thr Thr Met	
45	1 8 10 15	
	(2) INFORMATION FOR SEQ ID NO:87:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LEWOTH: 15 amino acids (B) TYPE: emino acids (C) STRANDENNESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	

Als Asn Leu Gin Sly Ile Sly Thr Thr Met Asn Ala Gis Asn Ala 8 1.0 (2) INFORMATION FOR SEC ID NO:88: 5 (i) SEQUENCE CHARACTERISTICS: (A) LEMOTE: 15 amino acida (B) TYPE: amino acid (C) STRANDEDNESS: single 10 (D) TOPOLOGY: linear (ii) NOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88: 15 The Gly Thr Thr Men Asn Als Gin Asn Ala Ala Ala Ala Ala Pro 1.0 (2) INFORMATION FOR 880 ID NO:89: 70 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (S) TYPE: amino acid (C) STRANDEDNESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SHOOMNCH DESCRIPTION: SEC ID NO:89: 30 Asn Ala Cln Asn Ala Ala Ala Ala Ala Pro Thr Thr Glv Val Val 1 8 (2) INFORMATION FOR SEC ID NO.98: 33 (1) SECURNCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amine soid (C) STRANDEDNESS: single 40 (D) TOPODOGY: linear (11) MOLECULE TYPE: pentide (xi) SECUENCE DESCRIPTION: SEC ID NO: 90: 45 Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp (D) IMPORMATION FOR SEQ ID NO:91: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scida (8) TYPE: amino acid (C) STRANDEDWESS: single 55 (D) TOPOLOGY: linear (ii) NOLSCULE TYPE: peptide

(xi) SECUENCE DESCRIPTION: SEC ID NO:9): Thr Thr Gly Vel Yel Pro Ala Ala Ala Asp Glu Val Ser Ala Seu 8 1.0 5 (2) INFORMATION FOR SEQ ID NO:92: (1) SEQUENCE CHARACTERISTICS: (A) LENGTW: 15 amino acids 16 (B) TYPE: amino acid (C) STRANDEDNESS: simple (b) TopoLOGY: linear (ii) MOLECULE TYPE: peptide 15 (%) SEQUENCE DESCRIPTION: SEQ ID NO:92: Pro Ala Ala Ala Asp Glu Val Ser Ala beu Thr Ala Ala Gln Phe 10 20 (2) INPORMATION FOR SEQ ID NO:93: (i) SEQUENCE CHARACTERISTICS: (A) LENGTE: 15 amino scids 25 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: Glu Val Ser Ala Leu Thr Ala Ala Gln Phe Ala Aia His Ala Gln 1 5 1.0 35 (2) INPORNATION FOR SEC ID NO: 54: (1) SEQUENCE CHARACTERISTICS: (A) LENGTE: 15 amino acids 40 (B) TYPE: amino acid (C) STRANDEDNESS: sincle (b) TOPOLOGY: Linear (ii) MOLECULE TYPE: peptide 45 (xi) SEQUENCE DESCRIPTION: SEO ID NO:94: Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr Val 2.0 3.5 56 {2} INFORMATION FOR SEQ ID NO:95: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 55 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
- 5 Als Als Als Als Gln Met Tyr Gln Thr Val Ser Als Gln Als Als 1 5 16 18
  - (2) IMPORMATION FOR SEC ID NO:96:
- 10 (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acida
  - (B) TYPE: amino acid
  - (C) STRANSELNESS: single
  - (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: peptide
  - (xi) SROUBNCE DESCRIPTION: SEO ID NO:96:
- 20 Met Tyr Gln Thr Val Ser Alz Gln Ala Ala Ala Ile His Glu Met Phe
  - (2) INFORMATION FOR SEQ ID NO:97:
  - 25 (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
- (D) TOPCLOGY: linear

45

- (ii) MOLECULE TYPE: peptide
  - (xi) SECURNCE DESCRIPTION: SEC ID NO:97:
- 35 Ser Ala Gin Aia Ala Ala Ile His Giu Mec Phe Val Asn Thr Leu 3 5 15 15
  - (2) INFORMATION FOR SEQ ID NO:98:
- 40 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
  - (3) TOPOLOGY: linear
- (ii) WOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEO ID NO.98.
- 50 Ala Ile His Glu Met Phe Val Asn Thr Leu Val Ala Ser Ser Gly 1 5 10 15
  - (2) INFORMATION FOR SEQ ID NO:99:
    - (1) SECUENCE CHARACTERISTICS:
      - (A) LEWGTH: 15 amino soids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS: single

	(D) TOROGOMY ILBRAI
	(ii) MOLECTIE TYPE: peptide
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
	Phe Val Asp Thr Leu Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr
	1 5 10 18
10	(2) INFORMATION FOR SEQ ID NO:100:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LEMOTH: 15 amino acida
	(B) TYPE: amino acid
15	(C) STEANDEDNESS: single
	(D) TOPGLOGY: linear
	(11) MOLECULE TYPE: peptide
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
	Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Aso Ala
	1 5 10 15
25	(2) IMPORMATION FOR SEQ ID MO:101:
	(i) sequence characteristics:
	(A) LENGTH: 14 amino soids
	(B) TYPE: smine scid
30	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide
35	(%i) SEQUENCE DESCRIPTION: SEQ ID NO.101:
	Ser Tyr Ala Als Thr Glu Ala Ala Ass Ala Ala Ala Ala Gly
	1 5 10
40	(2) INFORMATION FOR SEC ID NO:302:
	(1) SEQUENCE CHARACTERISTICS:
	(A) LENOTH: 1784 base pairs
0.20	(B) TYPE: nucleic acid
45	(C) STRANDEDTESS: #ingle
	(D) TOPOLOGY: linear
	(11) MOLECULE TYPE: CDMA
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
	ATTCOTTCCT QCORGAGCTA MATCCORGOR ACMTCGTCGC CGGCCMGTAC GAGGTCAAAG 60
	GCTGCATCGC GCACGGOGGA CYGGGCTGGA TCTACCYCOC TCTCGACCGC AATGTCAACG 120
	GCCGTCCGGT GGTGCTCLARG GGCCTGRTGC AFTCCGGTGA TOCOCAAGGG CAGGCAATUG 180
55	CHATGGCOGA ACCOCACTTC CTGGCCGAGG TGGTGCACCC GTCGATCGTG CAGATCTTCA 240
	ACTITICA GCACACCAC ACCCACAGO ATTOCCTO CTACATCAT ATGGAATACC 300

TOGGCGGGCA ATOGCTCAAA COCAGCAAGG GTCAWAAACT GCCCGTCGCG GAGGCCATCG

CUTACCTUCT GGAGATCCTG CCOGCGCTGA GCTACCTUCA TTYNATCGGC TTOGTCTACA

360

ACGACCTOAA GCOCOSTATC CCGAGATCOST TCGCGGCGCCT AMERICIACCC TSTTGCGGGA AGTCCCAGTC	GCGGACCGGT CACGCTGGAC GGTGCTGAAA GCGGCAACGG	TOOTTOGGET CCGACGOTGO CTGCCCACCC	CCGAGGAACA ACCTCTACGG CURCOGACAT GCAATGGCCG CTTACGGCCG	GCTCAAGCTG GACCCCAGGC CTACACCGTG TTATGTGGAT GTTGCTGCGC	TTCCAGGCCC GGACGCACGC GGGCTACCCG	480 540 600
CCGAGATO9Y TCGCGGGGGT AAGACGACCC ACCCGATCC TGTTGCGGGA	GCGGACCGGT CACGCTGGAC GGTGCTGAAA GCGGCAACGG	CCGACGGTGG CTGCCCACCC ACCTAGGACT	CUACOGACAT GCAATGGCCG	CTACACCGFG TTATGTGGAT	GGACGCACGC GGGCTACCCG	690
TOGOGGGGT AAGAGGAGCC AGGGGGATGC TGTTGGGGGA	CACGCTGGAC GGTGCTGAAA GCGGCAACGG	CTGCCCACCC ACCTAEGACT	OCANTGGCCG	TTATGTGGAT	GGGCTACCCG	
AAGROGADOO ACCOCCATOO TGTTGCGGGA	GGTGCTGAAA GC88CAAC88	ACCTACGACT			And the following the state of	650
ACCCCCATCC TGTTGCGGGA	GCGGCAACGG		CTTACOGCOG	approximate		
TGTTGCGGGA		TTCACCACCG			AGGGCCATCG	720
	COTTOGTCGCC		CCGAAGAGAT	OTCCGCGCAA	TTWACGGGCG	780
AGTCCCAGTC		CAGACACCGG	GGTGCCGCGG	CCAGGCTATC	AACGATCTTC	846
	OSTOGACATE	TGGAGTGGAC	TECTOGTOGC	GCACACOGAC	GTGTATCTGG	900
ACCCCCACCT	GCACGCGGAG	AAGCTGACCG	CCAACGAGAT	COTGACCGCG	CTGTCGGTGC	960
COCTCOTCOA	TCCGACCGAC	GTCGCAGCTT	COSTCCTCCA	OGCCACOGT/3	CTCTCCCAGC	1630
CGGTGCAGAC	CCTAGACTOS	NTGCGCGCGG	CCCSCCACGG	TGCGCTGGAC	GCCGACGGCG	1080
TOGATTHTOC	GAGTCAGTOG	AGCTGCCGCT	AATGGAAGTC	CGCGCGCTGC	TEGATCTORG	1140
COATGTGGCC	AAGGCCACCC	GARRACTCGA	CGATCTGGGC	GAACGCGTTG	OCTOGCOATO	1230
GOGATTGGTC	TGGTACCGGG	COGTOGCOGA	GCTGCTCAOC	GGCGACTATG	ACTCGGCCAC	1260
CAAACATTTC	ACCGAGGTGC	TOGATACCTT	TOCCGGCGAG	CTGGCGCCCA	AGCTCGCCCT	1320
0000000CACC	GCCGAACTAG	COGGCAACAC	COACGAACAC	AACTTCTATC	AGACOGTSTG	1380
GAGCACCAAC	GACGGCGTGA	TCTCGGCGGC	TTTCGGGACTG	SCCAGAGGCC	GGTGGGGCGGA	1440
AGGTGATCGG	GTOGGGGGGG	TOCGCACGCT	CGACGAGGTA	CCGCCCACTY	CTCGGCATTT	1500
CACCACGGCA	CGGCTGACCA	GCGCGGTGRC	TUTGTTGTCC	GGCCGGTCAA	CGAGTGAAGT	1560
CACCGAGGAA	CAGATYCCGCG	ACCCCCCCC	AAGAGTGGAG	GCGCTGCCCC	COACCUARCC	1626
ACGORTGCTG	CAGATCCGCG	cccraaracr	GGG7/3GC3CG	CTGGACTGGC	TGAAGGACAA	1680
CAAGOCCAGC	ACCAACCACA	TOCTOGGTTT	CCCOTTCACC	AGTCACGGGC	TGCGGCTGGG	1740
TGTCGAGGCG	TCRCTGCGCA	<b>GCCTGGCCCG</b>	GGTAGCTCCC	ACTC		2784
CO W. A. M. A. M. C. W. M. A. M. M. A. M.	OGGTGCAGAC TOGATTTTCC TGATGTGGCC TGATGAGTGATTTC TGATGACACT TAGACACTAC TGATGATCGC TGATGACC TGATC TGATGACC TGATC TGATGACC TGATC TGA	TORTHOGRAM COTHARATOR TORTHYTO GRATCHOTOR TENTITION RAMISCANCES TORTHYTOT TOTH TOTH TORTHOGRAM THANACHTTE ACCAMPINE THEORY TOTH TOTH TOTH TOTH TOTH TOTH TOTH TOT	DEFICABAR COTABACTOS MTRUCUCAGO TOSATITICO CONTROLO CONTROLO CARTOCATOR ASCITACIONE ASCITA	DESTRICABAR COMBARCTOS MINICESSOCIS OCODOLADOS FORDATINHOS CARTORISMOS ACONSCIONES ARXIGUARNIO EMPLOYMENTE TESTRICOSO COMPOSICIA, CONTOCTISCO DELACATITE ACCASOTOS COMPOSICIA, CONTOCTISCO DELACATITE ACCASOTOS TOMATACTIT TOCCOSCOSIA BIOCOSCIACO GIOCOSANCINA TOTOSICOSO TOTOSICIANO REPORTACIONE GIOCOSCITA TOTOSICOSO TOTOSIAGONO REPORTACIONO GIOCOSCITA CONTOCIONO DELOCATOSICO CONCENTRA CONTOCIONO DELOCATOSICO CONCENTRA CONTOCIONO DECORDISCO COMPOSITICO CONTOCIONO DECORDISCO CONTOCIONO DECORDIN	DESTRICAGIAS COMBARATOR MUSICAGUAGO COMBORADA TROGUTAGRA PROGUTAGRA PROGUTAGR	CRETICAGAR CYTAGACTOS MINICESCOS COSCOLARSE INSIGERSOR GOGARDECE FORATTIFICO GARTCARTOS GACUNCOCCE TARIORAMIC COGOGOGOTO COGOGOGO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGOTO COGOGOGO COGOGOGO COGOGO COGOGOGO COGOGO COGO COGOGO COGO COGOGO COGO COGOGO COGO COGOGO COGO COGOGO COGO CO

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- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 766 base pairs

  - (8) TYPS: smeleic acid (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DDNA
- 35 (x1) SEQUENCE DESCRIPTION: SEQ LD NO:103:

	ACAARACACT	CGGYGGCKGC	CONTOCUOCC	TUATCGTCGG	TGATCAGCYT	COTOCCAARY	60
	TOGGCACAAG	OTOCOCOCTR	CCCAANGAGT	TOTTCGCCGC	ROTGOGMGCM	KAACTGGCCT	120
	ATCNTGGTTG	GGTGCCGTCC	<b>COCANAACCC</b>	GCUAACTTAA	ACCCATTITA	ACCOMMENDE	180
40	AAGTTTCCTA	CATYTACCCM	RGSMANCCAA	COGGGCCGCC	MANAAMTCCG	TCCTGGANTC	240
	CGANCGGTTC	CCGGTGTTCG	COGCACTGCT	GACCGGCACG	GARTATOCGC	AGGCGCCGTT	300
	GGCCAACGCG	TOCOTOCAAC	TOGCCTACGG	TGCGCACCAS	GACGCCATCA	CCGGCTCGGA	360
	GICCGACCAG	GTACTCAATG	CTGGCGACCA	CACCACCCAG	CAGACCAAAC	TGGTGCACGC	420
	CGATCTCCAG	GEGCGCCGGC	COGGTGGCAT	ACCOATTOOT	CGAAACCAAT	COGAAGGAAT	480
45	TCATCACOGA	COGTUACURA	AAACGATCGC	CCCAATGGGN	GGACWACCON	Addicagodin	540
	ATTHACCOTT	NAACAAGTTG	CNGTAGGTTC	TITGATATCG	AKCAACCGAT	ACCIGATION	660
	CCGCGGAATG	GTAGACCACC	ACCACTRICEC	NCAMGINGIG	CACCAGTTTG	GTCATCOCCC	550
	SCAGATCGGT	GACCCCGCCA	AGCOTTCCOG	ATGCGGAGAT	GASGGTGACC	AGCCYGGTTG	720
	ACCTOTTGAT	CAGGTINTCC	CAGTGCCACG	TCGGCAGCTG	occorr		766
50							

- (2) IMPURMATION FOR SEQ ID NO: 104:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1231 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOUSCOLE TYPE: CDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID 80:104:

5	CGGCACGAGA	ATGTCGCCTG	TGCCTCGATA	GCCACTTGCG	TGTGGTCGCG	CTGCCAGCSG	60
	GTCAGCCAGG	TOSCCTGGTC	CAGGCCATCG	GGCCGGCGCA.	GGAGCGCGAT	GTTSGCCRGA	120
	CCCGGTGTAC	GAGAACCGGA	CTCGACMAAG	TOTOGGGGGGT	GACGGGGGGGT	CACFTCGCGG	180
	CACACGCCCA	GATCTATCAG	<b>GCCGTCAGCG</b>	CCCAGGCCGC	OGCGATTCAC	GAGATOTTCO	246
	TCAACACTCT	ACAGATNANC	TCAGGGTCGT	ATOCTGCTAC	CGAGGCCGCC	AACGC09GCC9	300
10	COOCCOOCTA	GAGGAGTCAC	TOCGATOCAT	TTTGGGGGGGT	TGCCGCCGGA	GGTCAATTCQ	350
	GTGCGGATGT	ATOCCGGTCC	TOGCTOGGCA	CCAATGGTCG	CTGCGGCGTC	GGCCTGGAAC	420
	ggg/reggcog	COMAGCTGAG	TTCGGCGGGCC	ACCOCUTTATO	AGACGGTGAT	CACTCAGCTC	489
	AGCAGTGAGG	GGTGGCTAGG	TOCGGOGTCA	GCGGCGATGG	CCGAGGCAGT	TROROGETAT	940
	GTGGCGTGGA	TWAGTGCCCC	TOCOGGGGGAA	GCCGAGCAGG	COGCCACACA	GGCCAGGGCC	600
15	GCCGCGGCCG	CTTTTGAGGC	<b>GGCGTTTGCC</b>	GCGACGGTGC	CTCCGCCGTT	GATEGOGGCC	660
	AACCGGGCTT	COTTGATGCA	GCTGATCTOG	ACCIDATOTOT	TTOTTCAGAA	CACCTCCOCO	720
	ATCGCGGCCG	CCGAAGCTCA	GTACGGCGAG	ATMT000CCC	AAGACTCCCC	OCCUPATOTAT	786
	GCCTACGCGG	GCAGTTCGGC	GAGCGCCTCG	GCGGTCACGC	COTTTAGCAC	GCCGCCGCAG	840
	ATTGCCRACC	CGACCGCTCA	GGGTFACGCAG	GCCGCGGCCG	YGGCCACCGC	CGCCGGFACC	900
20	OCCCAGTORA	CGCTGACGGA	GATGATCACC	GGGCTACCCA	ACCCCCTCCA	AAGCCTCACC	960
	TCACNTCION	TGCAGTCGTC	TAACGGTCCG	CTGTCGTGGC	TGTGGCAGAT	CTTGTTCGGC	1020
	MOSCCCAATE	TOCCCACCTC	AATTTCGGCA	CTGCTGACCG	ACCTGCAGCC	CTACGCGAGC	1080
	TTETTETATA	ACACCGAGGG	CCTGCCGTAC	TTCACCATCO	GCATGGGCAA	CAACTTCATT	1140
	CASTOSGCCA	AGACCCTGGG	ATTGATCGGC	TAGGCGGCAC	COCCTOCOST	CHCGGNTGCT	1230
25	GGGGATNCCG	CCAAGGGCTT	GOCTCGTGCC	G			1231

## (2) INFORMATION FOR SEC ID NO:105:

- (i) SEQUENCE CHARACTERISTICS: 30 (A) LENGTH: 2041 base pairs
  - (B) TVPE: nucleic soid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Linear
- 35 (ii) MOLECCUR TYPE: CDNA

	(x1)	SEQUENCE D	BSCRIPTION:	SEC ID NO:	L05:		
	COOCACCAGC	TCSTGCOSAT	CACTGCCATT	GACGGCTTGT	ACGACCTTOT	CCCCATTOGA	60
40	ATACCCAACC	AAGGGGGTAT	CCTTTACTCC	TCACTAGAGT	ACTTOGRASA	ACCCCTGGAG	120
	GAGCTGGCAG	CAGCGTTTCC	GGGTGATGGC	TOGTTAGGTT	CGGCCGCGGA	CAAATACGCC	180
	<b>GGCAAAAACC</b>	GCAACCACGT	GARTTTTTC	CAGGAACTGG	CAGACCTCGA	TOSTCASCTC	240
	ATCAGCCTVA	PCCACGACGA	OCCCAACGCG	GTCCAGACGA	CCCCCCGACAT	CCTGGAGGGC	300
	GCCAAGAAAG	GTCTCGAGTT	COTGCGGGGG	GIGGCTGTGG	ACCTOACCTA	CATCCCCGGTC	360
45	GTCGGGGCACG	CCCTATCGGC	COCCTTCCAN	COSCOSTITT	acacagacac	GATGGCCGTA	420
	grougcodes	CGCTTGCCTA	CITGGTCGTG	AAAACGCTGA	TCAACGOGAC	TCAACTCCTC	480
	AAATTGCTTG	CCAAATTUGC	GGAGTTGGTC	GCGGCCGCCA	TTGCGGACAT	CATTTOGGAT	540
	GTGGCGGACA	TOATCAAGGG	CATCCTCUGA	CONFOTORAD	AGTICATURC	AAACGCCCTC	500
	AACGGCCTGA	AAGASCTTTS	GGACAAGCTC	Acooograde	TOACCGGACT	GITCICTOGA	880
50	GGGTGGTCGA	ACCTGGAGTC	CTTCTTTGCG	GGCGTCCCCG	GCTTGACCGG	CGCGACCAGC	720
	COCTTOTOGC	ANGTOACTOG	CTTGTTCGGT	GCGGCCGGTC	TOTOCOCATO	OTCOGGCTTG	780
	GCTCACGCGG	ATAGCCTGUC	GAGCTCAGCC	ACCTTGCCCG	CCCTCGCCGG	CATTGGGGGC	840
	GGGTCCGGTT	TTGGGGGCTT	GCCGAGCCTG	GCTCAGGTCC	ATGCCGCCTC	ARCTCGGCAG	900
	GCGCTACGGC	CCCGAGCTGA	TRACCOGGIC	OCCOCCOCTO	CCGAGCAGGT	CBBCBGGCAG	960
55	TOTCAGCTGG	TCTCCGCGCA	GGGTTCCCAA	GGTATUGGCG	GACCCGTAGG	CATOGGCGGC	1020
	ATGCACCCCT	CTTCGGGGGGC	CINCGAAAGGG	ACGACGAGGA	AGAAGTACTC	GEARGGCGCG	1080
	GCGGCGGGCA	CTGAAGACGC	CGAGCGCGCG	CCAGTCGAAG	CTGACGCGGG	CGGTGGGCAA	1140
	AAGGTOCTUG	TACGAAACST	COTCTAACGG	CATGGCGAGC	CARATCCATT	GUTAGCCAGC	3200

CORRECCIONA CONTROLLE TRANSCRICTOR CORRECTATOR ARCOCOSCOS TRANSCRICTOR CORRECTOR TO ACCOUNT TO THE TRANSCRICTOR CONTROLLE		GCCTRACAAC	GOSCAATGOY	AAACOGAAGG	GACACGATCA	ATGACGGAAA	ACTIGACOGY	1260
CTOCTOCACAS   TICALCAGE   COTTALATOR   GENETICACT   GEOGRAPH   GENETICACTOR   TRACKSARGE   GAUGRAPH   GENETICACTOR   GRACKSARGE   GROUNDAGE   GAUGRAPH   GENETICACTOR   GRACKSARGE   GAUGRAPH   GENETICACTOR   GRACKSARGE   GAUGRAPH		CCAGCCCGAG	COTCTCOOTG	TACTGGCGTC	GCACCATGAC	AAC9C0GCGG	TOGATGOMTO	1320
5 GTCCTTGGAT ACGGCCGGTG TCGARCTIGG CRAAGGTTT GGAATTGGGG CGAAGGTTT TGGAGGCCGCG TGCGAGGT TGCGGCGCGCG TGCGAGGT TGCGGCGCGCGGT TGCGAGGTT GGAGGCGGGT TGCGCGCGCGGT TGCGGGGTGGGGGGGGGG		CTCGGGGGGTC	GAAGCTGCCG	CTGGCCTAGG	CGAATCTGTG	GCGATCACTC	ACCOTTOCTA	1380
TARRESHORE GROUNDAMOUNT GOUGHAGUE TERREACOGO TEOTETRICE GROCACOTTT   150		CTGCTCACAG	TTCAACGACA	COTTABATOT	GTACTTGACT	GCCCACAATG	CCCTOGGCTC	1440
GUTGCCCCCA GTCCAGGCCA GGACGTACCG CAGTCCGTCC CATCCCTAGG CGTCGAGGCCAC CACCCCCCATC ACCOCCCAC CATCCCCACAC CACCCCCCACAC CACCCCCCCC	5	GTCCTTGCAT	ACGGCCOGTO	TOGATCTCGC	CAAAAGTCTT	CGAATTCCCC	COAAGATATA	1500
ACCIGICAGE ACCIDENCES   1680		TAGCGAGGCC	GACGAAGCGT	GOCGCAAGGC	TATCCACGGO	TIGITTACCT	GACCACGTTT	1550
DECONCEGACIO GETTORISSEA CARACCERISCI CROFFERRICO TROCOGCACIO CONTROTRORIO 1740  GORGOCICARIO COCOGRAGOS CONTRALACEA TECNORICOCIA GEOGRACIA GETTORISCOSI 1860  TECCIONATO COCOGRAGOS CARCARDACEA COCOCORACIO GEOGRACIA GETTORISCOSI 1860  TECCIONATO TRADATACTE COMPANIANO COCOCOCACIO GEOGRACIA GETTORISCOSI 1860  ATUGITARIO COCOCTINISTI GEORGACIA CORCOCOCACIO GEOGRACIA GETTORISCOSI 1860  ATUGITARIO COCCUTARISTI GEORGACIA CORCOCACIO GEOGRACIA GEOGRACIA GEOGRACIA GEOGRACIA GEOGRACIA GEOGRACIA GEOGRACIA GEOGRACIA COCOCCUTA GEOGRACIA GEOGRAC		GCTGCCCGCA	GTGCAGGCCA	CGACGTAGCG	CARGITCOTOT	CCCTCGTAGG	COTOGATOCO	1620
OGRACCICAR COCCICACION CONTINUATE TECCARCICO AGENCIACIO AGANCTORTO   TEGECOARIC COCCICORNO CARCIONATO CIRCARCO AGENCIACIO TETECOARIC COCCICONATO CONTINUATORIO DE PARTICIPA TRADATATA CONTINUATORIO DE PARTICIPA TRADATATA CONTINUATORIO COCCICORNO CARCIONATORIO COCCICORNO CARCIONAL COCCICORNO		ACCORDCARC	ACCAGCACCC	GOTGCGCACC	GATGGGCACG	GACAGTAGCT	CGCCCGCATG	1.680
TTGGCGANC COGNOGOST GARCAGNACA CTGGGGGCGC GGCCGGGGGGA GTTTGTGGGGGA TTGGGGGGGGGG		CCCGGCTGCG	GTTGGC99CA	CARACCCGGG	CAGTTCGGCC	TGCGGCAGCA	COGTOGTMOG	1740
ATCEGEGEGE GENTRACTER SCHOOLSE SCHOOLSE SCHOOLSE SERRESCHES 1920 TRUTHERSEEN TRUSHINGTON CONTROLLED TO THE SEQUENCE ACCOUNTS CONTROLLED TO THE SEQUENCE CONT	10	GGAGCCCARC	GCCGCAACQG	CCGFFFAACCA	TCCCGACCCG	AGCACGACCG	AGACGTCATG	1800
TUCTHORICES TRAGSTATES GRAGETES AGENCICAS CATECORCE GRETCARORS 1580 ATTOSTEGIC GROCCHEST GRAGETEST GRACETESC CATECORTEC ACCTOSTICS 2041  (2) INFORMATION FOR SEQ ID NO:106;  (i) SEQUENCE CHARACTERISTICS; (A) LENDTH: 1202 base pairs (B) TIPH: mccleic acid (C) STRAMBENIESS: single (D) TOPOLOSY: linear  25 (ii) MOLECULE TYPS: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106;  GAGCTOACCC CTATCARCCA ATACTFTCTS CAUTCLARGA TSCAGGACCA CTGGGGTTTT ACCGGGGCARCA CGGCCARGAA TACTFTCTS CAUTCLARGA TSCAGGGCACA CTGGGGTTTT ACCGGGCARCA CGGCCARGAA TACTFTCTS GRAGETEST CGGCCARCA TROTTCARGA TSCAGGCACA CGGCCARGAA TACTFTCTS GRAGETEST TSCAGGCA TACCARGAT CGGCCARGA TACTGGGGTT TTTATATACOTT CTAACACCA ATACTFTCTS GRAGETEST TSCAGGCAACT ACCGGACCA GRAGETEST TSCAGGCA GRAGETEST TSCAGGCA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACA GRAGETEST TSCAGGCACACA GRAGETEST TSCAGGCACACACACACACACACACACACACACACACACAC		TTCGCCGATC	CCGGTGCGGT	CAGCGATGAC	ergogecoec	CGCCGGGCCA	GITTOTCOGG	1850
ATTOUTNESS GOCCOTHESTS GOGAGCTOST GRAGCTOTCC CATGCCATCC ACCTOSTOCC 2040  (2) INFORMATION FOR SEQ ID NO:106;  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANBERHESS: single (D) TOPOLOGY: linear  25 (ii) NOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SED ID NO:106;  (GAGCTCACCO CHATCARGCA ATACTPTCTO CACTCCARGA TECANGGACA COCCEGAGAA 138 ACCARACTOC GOGCCACAC COCCAGAGA TECANGGACA COCCEGAGAA 138 ACCARACTOC GOCCCACAC COCCAGAGA TECANGGACA COCCEGAGAA 138 ACCARACTOC GOCCCACAC COCCAGAGA TECANGGACA COCCEGAGAA 138 ACCARACTOC GOCCCACAC COCCAGAGA TECANGGACA COCCEGAGAA 138 ACCARACTOC GOCACCACAC COCCAGAGA TECANGGACA COCCAGAGACAC COCCAGAGACAC COCCAGAGACAC COCCAGAGACAC COCCAGAGACAC TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGACAC COCCAGACAC CACCAGAGACAC COCCAGACACAC CACCAGAGACAC COCCAGACACAC CACCAGAGACAC TAGAGAGAGAGACA TAGAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACA TAGAGAGAGACAC TAGAGAGAGACAC TAGAGAGAGACAC TAGAGAGAGACAC TAGAGAGAGACAC COCCAGACACAC CACCAGACACC CACCAGACACC CACCAGACAC CACCAGACAC CACCAGACACAC TAGAGAGAGAGACAC TAGAGAGAGAGACAC TAGAGAGAGAGACAC TAGAGAGAGACAC TAGAGAGAGAGACAC TAGAGAGAGAGACACC CACCAGACACC CACCAGACCACACCACC CACCAGACCACC CACCACACCACC CACC		ATCGGGGGGG	GGGTCAGCCA	CACTGGGCGA	GCTTAACTGA	GCCGCTCGCC	GOGGAGCGGG	1920
15   G   2043		TUCTNOTCOA	TGAGATACTG	COMBCATOCC	AGCAGCCAGC	GCATCCGACC	CCCTCCAOCA	1980
(2) INFORMATION FOR SEQ ID NO:106;  (i) SEQUENCE CHARACTERISTICS; (A) LENGTH: 1202 base pairs (B) TYPH: Nucleic acid (C) STRANDEDHESS: single (D) TOPOLOGY: linear  25 (Ai) NOLECULE TYPE: cDNA  (Xi) SEQUENCE DESCRIPTION: SED ID NO:106;  GAGCTACCO CTATCARGCA ATACTTTCTO CACTCCARGA TECARGACAC COGGOGTTT ACCCURACY COATCARGCA ATACTTTCTO CACTCCARGA TECARGACAC COCCORGAGA 128 ACCGARGTGG COGCOCACC COCCORGAGA TECARGACAC COCCORGAGA 128 ACCGARGTGG COGCOCACC COCCORGAGA TETOLOGACA ACCRAGACAC COGGOGTA TYBRANCOIN: TRANSCORD AATCCTTCATA TUCCAGGAGAA ACCAGGAGAC COCCAGGAGAC TYBRANCOIN: TRANSCORD AATCCTCATA TUCCAGGAGAGAACACAC COCCAGGAGACACACACACACACACACACACACACACACA		ATTGGTGCGG	CUCCUTGGTG	GCGAGCTOGT	CGAGCTGTCC	CATGCCATCC	ACCTCGTGCC	2049
(i) SEQUENCE CHARACTERISTICS; (A) LENGTH: 1202 base pairs (B) TYPE: mucleic acid (C) STRANMENESS: single (D) TOPOLOGY: linear  25 (ii) MOLECULE TYPS: cDNA (Ai) SEQUENCE DESCRIPTION: SED ID MO:106:  GAGCTOROCG CTRATCRACCA AFACTITICTS CACTICOARGA TECROGRACIA CTGGGGTTTT 50 ACCGRACGG COARCCACA COGGGGGGG TOSTTOGRACG AFATCOROCA CGCCCARGA 120 ACCGRACGGG COGGCCACAC COGGGGGGG TOSTTOGRACG AFATCOROCA CGCCCARGA 120 ACCGRACGGG COARCCACCA COGGGGGGG TOSTTOGRACG AFATCOROCA CGCCCARGA 120 ACCGRACGGGG COARCCACCAC COGGGGGGG TOSTTOGRACG AFATCOROCAC CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	15	G						2043
(a) INNOTH: 1202 base pairs (b) TYPE: mucleic acid (c) STRANDENIESS: single (d) TOPOLOGY: linear (d) TOPOLOGY: CANCELOGY: CONTROL TOPOLOGY: TOPOLOGY: COCCERGUAL COCCER		(2) INFORMA	TION FOR SE	Q ID NO:106	,			
(a) INNOTH: 1202 base pairs (b) TYPE: mucleic acid (c) STRANDENIESS: single (d) TOPOLOGY: linear (d) TOPOLOGY: CANCELOGY: CONTROL TOPOLOGY: TOPOLOGY: COCCERGUAL COCCER		671		A A A A A A A A A A A A A A A A A A A				
(ii) TYPE: nucleic acid (c) STRAMBERHESS: single (d) TOPOLOGY: linear  25 (iii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SED ID MO:106:  GAGCTOACCU CTATCAAGCA ATACTFTCTE CACTCCAAGA TSCAGGACAA CTGGGGTTTT 60 ACCGAGGTGG GGGCCACAC COGCGGGGG TSCATTCGAGG ATACGGGCACA CGCCCAGGAA 126 ACCGAGGTGG CGCCCACACACACACACACACACACACACACACACAC	20							
(c) STRANDENIESS: single (d) TOPOLOGY: linear  25	200				21.0			
25 (11) MOLECULE TYPE: CONA  (x1) SEQUENCE DESCRIPTION: SED ID MO:106:  GAGCTOACCG CTATCARGCA ATACTTTCTG CACTCCARGA TSCARGACCA CTGGGGTTTT 50 ACCHAGGTGG CGGCCOACAC COCCOGGGG TSSTTTOGGGG AATTGGGGCA CTGGGGTTTT 70 ACCHAGGTGG CGGCCOACAC COCCOGGGGA TSSTTTOGGGG AATTGGGCA CGCCGAGGGA 120 ACCAGGGTGG CACTCTTGT GCGGGGATGGT TTGCCGACGAC ACCGGGCGGG ATACGGGCA CGCCGAGGAC ACCGGCC 34 TTGAATGGTG AGAAAATGGT TGCGGACGAG GAGGGGAGA TGGAGGAGGA GAGGAGGAG ATACGGGG ATACGGGC 35 CTGGAGGACTA TGGACAACAG AATTGCGG GAGGAGGAG ATACGGGGC GGCCACGAC ACCGGCC 34 CCGACCTGAT GCCCACTGA GAATGCGGG CTGCCACGAC CACGGCC 35 CTGGAGACGAG AGAAAATGGT TGCCGACAGA ATACGACGT GGACAACAG ACCGGCC 35 CTGGAGACGAG AGAAAATGGT TGCCGACAGA ATACGACGT GGACAACAG ACCGGCC 35 CCGACCTGAT GCCCACTGA GAATGCCGC GAGACACAG CACGACCAG ACCGACCAG ACCGAC								
(xi) SEQUENCE DESCRIPTION: SED ID NO:106:  GAGCTOACCE CTATCAACCA AFACTETICTS CACTCCAACA TOCAGGACAA CTGGGGTTTT 60 ACCGAGCAGCA COCCGAGGA ACCGAGCAGCA CGGCCAGGA ACCGAGCAGCA CGGCCAGGAA ACCGAGCAGCA CGGCCAGGAA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG								
(xi) SEQUENCE DESCRIPTION: SED ID NO:106:  GAGCTOACCE CTATCAACCA AFACTETICTS CACTCCAACA TOCAGGACAA CTGGGGTTTT 60 ACCGAGCAGCA COCCGAGGA ACCGAGCAGCA CGGCCAGGA ACCGAGCAGCA CGGCCAGGAA ACCGAGCAGCA CGGCCAGGAA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA ACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCA CACCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	25	(435	MOLECULE T	year obes				
GAGCTCACCC CTATCAACCA AFACTFTCTC CACTCCAAGA TSCAGGACAA CTGGGGTTTT 56 ACCGAGCTGG GGGCCACAC CGGGGGGGGA TCGTTCGAGA TSCAGGGGACAA CTGGGGGTTTT 66 ACCGAGCTGG GGGCCACAC CGGGGGGGA TCGTTCGAGA AAATCGGGCA CGCCCAGGAA 128 ACCGCAGCAC AGACCGCCC CGGGGGAGA TCGTTCGAGAC ACCGAGGGCA CGCCCAGGAC 128 OFFATCGGCC AGACCGCCC CGGGCAGACAC ACCGAGCCCC CGGGCCCACACACA								
		(X7)	REQUENCE D	ESCRIPTION:	SEQ ID NO:	1.06:		
### ATCHCOGNEC GENETITOTT GETGALTOST TETROCUALCY ACCARGODOST COGRETOSTO 398 DETRITOS CARACTERIST GETGALTOST TETROCUALCY ACCARGOSTOST COGRETOSTO 349 DETRITOSCO ACCARGOSTOST TETROCUALCY TROCORPITATA TRACOGRACIO ARTOSTOSTOST GENERAL ARTOGRACIO 240 DETRITOSCO ACCARGOSTOST CONTROLOGOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTO								80
09787CGSCC AGRACGECOG GUAGEAATT         GAGGCGATCT         240           TEGRATAGETC AGRACGEGO ARTOFERAT TOCCORDATE         240           TEGRATAGETC AGRACGEGO ARTOFERAT TOCCORDATE         240           35         CTGGAGACTAG ARTOFERAT         TOCCORDATE         350           CCGACCTGAT         GACCACTGAT         GACCACTGAT         360           AGCATCHATT         GCCCCCTTGA         GARTATCACCO         GACCACTGAT         480           AGCATCHATT         GCCCCCCCC         AGCATCACCO         AGCATCACCO         ACCACCTGAT         480           AGCATCACCO         CARTACCCCAC         CONTROLLOR         CONTROLLOR         CARCACTGAT         480           46         GACATTCCCCA         CARCACTGAT         CARCACTGAT         CARCACTGAT         480           AGCATTCCCCA         CARCACTGAT         CARCACTGAT         CARCACTGAT         CARCACTGAT         480           40         GACATTCCCCA         CARCACTGATC         CARCACTGATC         CARCACTGATC         CARCACTGATC         780           40         GACATTCCCCA         CARCACTGATCACCACCACCACCACCACCACCACCACCACCACCACCA	30	ACCGAGCTGG	CGGCCCACAC	COSCSCSSAS	TOSTTOGACS	AAATGCGGCA	COCCGAGGAA	120
TTORATORIC TOLARCUROS ARTOFICATE TOCOGGGRAS ALCARGANCA CACCAGOSCO 3.90 STATISTICO AGABANCOST TOCOGRAS CARAGANCAS TOLARCANOTA GRANAGONS 3.50 CTGGARCTIGAT TOGACAGAGC TOCOGRAS CARAGANCAS TOLARCANOTA GRANAGONS 3.50 CCGGCCCCCCC GRANAGONS AGARCTICO COCCAGONO ACCAGONO AC		ATCACOGATC	GCATCTTGTT	GCTGGATGGT	TTGCCGAACT	ACCAGCGCAT	COGTTCGTTO	189
STATISCIDIO AGAARATICOT TUCCURICULO GARGAGACAN TOGACTACTT GGALAGGOAG   360								240
		TTGAATCOTC	TYCAAGCCAGG	AATCOTCATG	TOUCGGGAGA	AACAGGAGAC	CACCAGCGCC	390
COGNOTION   GOCCOCTION GRATTETICO   ATRICACTICO   BRIDGECORT GRAAGETET   480								360
MCATCGACT	35							420
GCCCCACCG   GANTOCASAC   GOTTOCACCC   GTTCCACTC   GGTTCGACCC   GAACATATAT   690								480
TECROSCAC TENTOSTOGO GONCROSCO GUNDARCOS GUN								540
40   GCATTGCCBA CBATGGTGG CBAGTGBGG AGCACCGTTD ACCASTCGTG GGCGGTCAGC AGCACTGTGAT ACCASTCGTG GGCGGTCAGC AGCAGTGCTG AGCAGTGTGAT TTCGGTCACC ACCTAGCGGC TGCCGGTGTG AGCAGTGCGA CCAGTGCGG TTCGTGGGGGG TTCGTGGGGGGT TTANTTGCGT TTANTTGCGT TGTTGGGTGTG ACCAGTGCGA ACCAGTGCGA CAGCAGTGGGG TGCTGGGGGGG AGCACCGCC AGCAGTGGGG AGCAGTGGGGGGGGGG								600
### ACCITATORUC TGGGGGGAC ACTERIGREE KTERKIERSE KERRRECTO GGTGATOTOC TGGGGGGC TGGGGGGGGGT TGGGGGGGGGGGG								660
TOUGGCORCAN CANOGETICITS   CTRAGETICITS   CTRAGET	40	CCATTGCCGA	CGATOGTCGC	CGAGCTGGGC	AGCACCGTTG	ACCAGTICGTO	GGCGGTCACC	720
GCGGTTATC   GCAGACGATG   ACCATOCTGG   CORPECTION   GGCGTCGGTG   950		AGCTATCTGC	TGGGGGGAAC	ACTOMYGNAK	KTGKKGKSKS	KERMRNKCTC	GGTGATCTOC	780
COGSTGGGST TYTOGFCACC GCCTACGGGC TGGCCGCTGS GSTGGTCCCA CTGCGGGGCC   960								849
45 GT000000TA COAGGGCOT TIANGTOLOG TOTTCOGTOT CAACACCGTC ACCGGTCOUC 10.20 TOTGGGGGG CTGGCTCACC GACKATCTGA GCTGGCGGCT GGGGTTCOAG CACALAGCCC CATCACCGGAC COCAGTGGGGG TCATCGGGGGC TGGGGGGGGGGG 10.00 TCCCTTGGGG AACGTGGTC CACAGCGCCA GAACGCTCGG AAATGCGAT GCCGACCCAC 12.00 AC 1202		GOGGGTTATC	GCAGACGATG	ACCATOCTOS	COATCTCTCC	OGCACTGCAG	GGCGTCGGTG	950
T9CT9GGGGG CTG9CTCACC GACTATCTGA 9CTBGCGGT GGGBTCCGA CLACLAGCCC 1090 CATCACCGAC CCGATCACGAC TCATCACGAC TCGGGGCGG 1190 CCGCCCTGGGGGGGG ACACGCCCC CTGGGGGGGGGGG								950
CATCACCGAC CCGATCGCGG TCATCGCGGG GAACACCGCC CTCGCGGGGT TGCGGGGAGG 1140 TCCCTTGGGG AACGTGGTCC CACAGCGCCA GAACGGTCGG AAATGCGATG GCCGACCCAC 1200 AC 1202	45	GTGGGGGGTA	CCAGGGGGGTC	TTANGTGCGG	TOTOCOGNOT	CAACACGGTC	ACCOGTOCGO	1020
TCCCTTGGGG AACGTGGTCC CACAGCGCCA GAACGGTCGG AAATGCGATG GCCGACCCAC   1200   AC   1202   50								1080
50 AC 1202		CATCACCGAC	CCGATCGCGG	TCATCGCGGC	GAACACCGCC	CTCGCGGCGT	TGCGGGCAGG	1140
50		TCCCTTGGGG	AACSTOOTCC	CACAGCGCCA	GAACGOTCGG	AAATGCGATG	GUCGACCUAC	1200
		AC						1,202
	50							

(2) IMPORMATION FOR SMO IN NO:107:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 496 base pairs
  - (B) TYPE: mucleic acid
- (C) STRANDEDNESS: single
- (D) TOPCLOGY: linear

(ii) MOLECULE TYPE: CONA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

5	GGCGGCGGCA	CTTOGCCAGC	AGTINGGGCG	GGGGAGCCGG	TTCGGNGACC	AAGAAATCOG	SC
10	CCTGGGCAAG	CAGCCGGGAC	CECCNACCUTT	GATCAGTING	GATCGCCGGG	ACCIGCOGCCG	120
	ACCAAMGCCA	TTCCGCCGNT	GAGGAAGTCG	GAARTRIGCO	CAGTGATGAC	GCCCTGCTGC	180
	AACGCNTOCC	GGATTGCCGA	GCGGATCGCC	GCCGAACGGC	GGTGCTCACC	ACCEGOGAGC	240
	ACCCCTACNG	ACAGGCCCGC	ATAGCTGAAT	SACGCCGGGT	NACOUCCUTC	CCWTCCACCG	300
	MGANATOGGC	CCGGANGCAA	AAGATCOGTC	GGCGCTCCGC	CTCGGCGACG	ACAGCCACGT	350
	TCACCCGCGC	GTTATCGGTG	GCCGCGATCC	CATACCAGGC	GCCGTCAAGG	TMGCCGTYGC	420
	GUTAGTCACG	CACCGACAAG	GTGATYTGGT	CCATCCCCTM	GAC00C0000	GYGACGCTGG	480
	CCCCCATCAM	OTOCAC					496

- 15 (2) INFORMATION FOR SEQ ID NO:108:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LEMOTH: 849 base pairs
- (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CENA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

	TOGATTCOGA	TAGCOGTTTC	GOCCCCTCGA	CGGGCGACCA	CGGCGCGCAG	GCCTCCGAAC	69
30	0000000000	GACGCTGGGA	TTCGCCGGGA	CCGCAACCAA	AGAACGCCGG	GTCCGGGGGG	120
	TOGGGCTGAC	COCACTOOCC	COTCATCACT	TCGGCAACGG	CCCCCGCATG	CCGATGGTGC	180
	COGGGACCTG	GGAGCAGGGC	AGCAACGAGC	CCGAGGCGCC	COACGGATCG	GGGAGAGGGG	240
	GAGGCGACGG	CTTACCGCAC	GACAGCAAGT	AACCGAATTC	CGAATCACGT	GGACCOSTAC	300
	OGGTCGAAAG	GAGAGATOTT	ATOMOCCTTT	TOGATGCTCA	TATCCCACAG	TYCOTGGCCT	360
	CCCAGTCGGC	STTTGCOGCC	AAGGCGGGGC	TEATGCGGCA	CACCLATCOUT	CAGGCOGAGC	420
35	AGGCGGCGAT	GTCGGCTCAG	GCGTTTCACC	AGGGGGAGTC	GTCGGCGGCG	TTTCAGGCCG	480
	CCCATGCCCG	GTTTGTGGCG	GCGGCCGCCA	AASTCAACAC	CTTGTTGGAT	GTCGCGCAGG	540
	CGAATCTGGC	TOAGOCCOCC	GOTACCTATG	TGGCCGCCGA	TECTGCGGCC	GCGTCGACCT	500
	ATACCOGGOTT	CYGATCGAAC	CCTGCTGACC	GAGAGGACTT	GTGATGTCGC	AAATCATGTA	660
40	CARCTRUCCC	GCGATGTTGG	GYCACGCCGG	GGRYATGGCC	COATATCCCC	GCACGCTGCA	720
	GASCTTGGGT	GCCGAGATCG	COSTOSAGCA	GGCCGCGTTG	CAGAGTGCGT	GGCAGGGCGA	780
	TACCGOGATO	ACGTATCAGG	COTGGCAGGC	ACENTGGTAA	CCANCCCANO	GRAGATTYGG	840
	TOCCOCCCT						849

- (2) IMPORMATION FOR SEQ ID NO:109:
- 45 (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
    - (xi) SECURNCE DESCRIPTION: SEC ID NO:109:
- 55 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser 1 5 10 15 Ala Pho Ala Ala Lys Ala Gly Leu Hot Arg His Thr Ile Gly Gln Ala 20 25 30

Glu din Ala Ala Mer Ser Ala Glo Ala Phe His Glo Gly Glu Ser Ser

Ala Ala Who Glin Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys 50 60

5 Val Asn Thr Leu Leu Asp Val Ala Gin Ala Asn beu Gly Giu Ala Ala 65 70 75 80 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly 95 95

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- (2) INFORMATION FOR SEC ID NO:110:
- (i) SEQUENCE CHARACTERISTICS: I5 (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
- Met Ser Leu Lou Asp Ala His Ile Pro Oln Leu Val Ala Ser Oln 25 1 5 10 15
  - (2) INFORMATION FOR SEQ ID NO:111:
    - (1) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 15 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS; single
  - (D) TOPOLOGY: linear
  - 35 (ii) WOLECULE TYPE: peptide
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
- Als His The Pro Gln Leu Val Als Ser Gln Ser Als Phe Als Als 40  $_{\rm 1}$   $_{\rm 5}$   $_{\rm 10}$   $_{\rm 15}$ 
  - (2) IMPORMATION FOR SEQ ID NO:212:
    - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino scids
      - (B) TYPE: amino acid
      - (C) STRANDEDWESS: single
    - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
- Let Val als ser Gin ser Ala Phe Ala Ala Lys Ala Gly Leu Met
  55 1 5 10 15
  (2) INFORMATION FOR SEC ID NO:113:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (b) TOPOLOGY: linear 5 (ii) MOLECULE TYPE: peptide (xi) SECTEMBER DESCRIPTION: SEC ID NO:113: 10 Ser Als Phe Ala Ala Lye Ala Cly Leu Met Arg His Thr Ile Gly 2.0 (2) INFORMATION FOR SEC ID NO:114: 19 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acida (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 20 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ XD NO:114: 25 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Als Glu Gln Ala 80 20 (2) INFORMATION FOR SEQ ID NO:115: 30 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS, single (D) TOPOLOGY: linear 35 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEC ID NO:115: 40 Arg Mis Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ber Ala Sln 2 36 1.5 (2) INFORMATION FOR SEQ ID NO:116: 45 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 dmino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 50 (iii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116: 55 Glm Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe Eis Gln Gly 1 1.0 (I) INPOPMATION FOR SEQ ID NO:117:

(1) SECURIOR CHARACTERISTICS: (A) LEMETH: 15 amino acids (B) TYPE: amino acid 5 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 10 (xi) SECURNCE DESCRIPTION: SEC ID NO.1174 Ala Met Ser Ala Gln Ala Phe His Gin Gly Glu Ser Ser Ala Ala 10 (2) INFORMATION FOR SEC ID NO:118: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino soid 20 (C) STRANDEDNESS: sincle (D) TOPOLOGY: linear (ii) MONECULE TYPE: peptide 25 (xi) SEQUENCE DESCRIPTION: SEC 10 NO:118: Ala Phe His Gim Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His 3 8 2.6 30 (2) INFORMATION FOR SEQ ID NO:119: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (B) TYPE: amino acid 35 (C) STRANDEDNESS: sincle (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 40 (xi) SEQUENCE DESCRIPTION: 880 ID NO:119: Glu Sex Sex Ala Ala Phe Gln Als Ala His Ala Aru Phe Val Ala 3 45 (2) INFORMATION FOR SEC ID NO. 126: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 smine acids (8) TXPE: amino acid 50 (C) STRANDEDMESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 55 (xi) SECRENCE DESCRIPTION: SEQ ID NO:120: Phe Gin Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val 20

	(2) INFORMATION FOR SEQ ID NO:121:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LEMOTH: 25 amino acids (B: TYPE: maino acid (C: STEANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) Wolacola TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID No:131:	
15	Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Lew Lew A	ap 5
	(2) INFORMATION FOR SEQ ID NO: 122:	
20	(i) SEQUENCE CHARACTERISTICO: (A) LENGTH: 15 mains acids (B) TYPE: amins acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear	
25	(11) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
30	Ala Ala Ala Lya Val Asn Thr Leu Leu Asp Val Ala Gin Ala A 1 5 5	on S
	(2) INFORMATION FOR SEQ ID NO:122:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LEMMIN: 15 mulho colde (B) TYPE: amino acid (C) STRANDEDWSSS: Single (D) TOPOLOSY: linear	
40	(ii) MOLECULE TYPE: peptide	
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 123:	
45	Asn Thr Leu Leu Asp Yal Ala Ghn Ala Asn Leu Gly Glu Als A	la 5
	(2) INFORMATION FOR SBQ ID NO: 324:	
50	(i) SEQUENCE CHARACTERISTICS; (A) LENGTH: 18 amino acids (B) TYPE: Maino acids (C) STRANDEDMESS: single (D) TOPOLOSY: linear	
55	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID SC:124:	

Val Ala Olh Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala 1 15 15 Asp Ala

- 5 (2) INFORMATION FOR SEQ ID NO:125:
  - (1) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1752 base pairs (B) TYPE: nucleic acid
- 10 /
- (C) STRANDEDNESS: single (D) TOPOLOGY: linesr
  - (11) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

	COGCACGAGA	ATGTYMCCTG	TUCCTOGATA	GCCACTIGCG	TGTGGTCGCG	CTGCCAGCGG	69
	GTCAGCCAGG	TOGGGTGGTC	CAGGCCATCG	GGCCGGCGCA	GGAGCGCGAT	GTTGGCCAGA	130
	CCCGGTGTAC	CAGAACCGGA	CTCGACWAAG	TOTCGGCGCT	GACGGCGGCT	CACTTCGCGG	186
20	CACACGCCCA	<b>GATCTATCAG</b>	GCCGTCAGCG	CCCAGGCCGC	GGCGATTCAC	GAGATGTTCG	260
	TCAACACTCT	ACAGATNANC	TCAGGGTCGT	ATGCTGCTAC	CGAGGCCGCC	AACGCGGCCG	300
	COCCCCCCTA	GAGGAGTCAC	TGCGATGGAT	TTTGGGGGCGT	TGCCGCCGGA	GOTCAATTCG	360
	GTGCGGATGT	ATGCCGGTCC	TOGCTCOUCA	CCRATUGTCG	CTGCGGCGTC	GGCCTGGAAC	420
	GGOTTGGCCG	COGAGCTGAG	Treggegge	ACCOUNTATO	AGACGGTGAT	CACTCAGCTC	480
25	AGCAGTGAGG	GGTGGCTAGG	TOCGGOGTCA	GCGGCGATGG	CCGAGGCAGT	TGCGCCGTAT	540
	GTCCCCTCGA	TGAGTQCCGC	TGCGGCGCAA	GCCGAGCAGG	CGGCCACACA	GGCCAGGGCC	600
	GCCGCGCGCGG	CTTTTSAGGC	SGCGTTTGCC	SCGACGGTGC	CTCCGCCGTT	GATCGOGGCC	660
	AACCGGGGCTT	CUTTGATGCA	GCTGATCTCG	ACGAATGTCT	TTOSTCAGAA	CACCTCGGCG	720
	ATCGCGGCCG	CCGAAGCTCA	STACGGCGAG	ATGTOGGCCC	AAGACTCCGC	GGCCATOTAT	780
30	GCCTACGCGG	SCAGTTCGGC	GAOCGCCTCG	OCCOTCACCC	CHTTTAGCAC	GCCGCCGCAG	840
	ATTGCCAACC	CGACOGCTCA	GGGTACGCAG	GCCGCGGCCG	TGGCCACCGC	CGCCGGTACC	900
	GCCCABTCGA	COCTGACGGA	GATGATCACC	GGGCTACCCA	ACGCGCTGCA	AAGCCTCACC	960
	TCACATCTGT	TOCAGTOSTO	TRACOGTOGG	CISTCSTGGC	TOTOGCAGAT	CTTGTTCGGC	1.020
	ACGCCCAATT	TOCCCACCTC	AATTTCGGCA	CTUCTGACCG	ACCTGCAGCC	CTACGCGAGC	1080
35	TINTINTATA	ACACCGAGGG	CCTGCCGTAC	TTCAGCATOS	<b>GCATGGGCAA</b>	CAACTTCATT	1140
	CAGTCGGCCA	AGACCCTOGG	ATTGATCGGC	TARROTTICAC	COGCEGCGGT	CROMMCTOCT	1200
	GOOGATGCCG	CCAAGGGCTT	GCCTGGACTG	GGCGGGATGC	TCGGTGGCGG	GCCGGTGGCG	1260
	GCGGGTCTGG	OCAATGOGGC	TTCGGTTGGC	AAGCTGTCGG	TUCCOCCOOT	OTGGANTGOA	3320
	COSTRECCOS	GOTCGGTTGAC	TOOGGGGGGCT	OCTCODCTAC	COOTGAGTAC	GOTCAGTGCC	1380
40	GCCCCGGAGG	CGGCGCCCCGG	ARGCCTGTTG	GGCGGCCTGC	CGCTANCESS	TECGGGCGGG	3440
	GCC9@CGCGG	GTCCACGCTA	COGATTCCRT	CCCACOUTCA	TGGCTCGCCC	ACCOPTOGNO	1500
	GOGRATAGECO	CTGCCGCAAC	GTATTAACGC	OCCOGCCTOS	OCTOSTOTOG	TECGETGOGG	1560
	STEGCAATTG	GTCMGCGCCG	AAATCTCSGT	GOOTTATTTE	CGGTGGGAZT	TTTTCCCBAA	1620
	GCCGGGTTCA	RCACCGGATT	TCCTAACGGT	CCCGCKACTC	YOUTOCCGAA.	TTCSGCACTA	1680
45	AGTGACGTCC	GOCGGARACC	COTTOGGINT	GAAAGCTTCA	GARAGOCCOG	CTCCCAGGGG	1740
	TTCOGCAAAC	33					1752

- (2) IMPORNATION FOR SEQ ID NO:126:
- 50 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTE: 400 amino acids (B) TYPE: amino acid
  - (B) TYPE; amileo acid (C) STRANDEDNESS; single
  - (D) TOPOLOGY: linear
- 55 ib; topology: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID BO:126:

```
Met Asp Phe Gly Ala Leu Pro Pro Glu Val Awn Sex Val Arg Met Tyr
                                   1.0
      Als Gly Pro Gly Ser Als Pro Met Val Ala Ala Ala Ser Ala Trp Asn
               20
                                 25
      Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
                              40
                                              45
      lle Thr Gln Leu Ser Ser Glm Gly Trp Leu Gly Pro Ala Ser Ala Ala
                          5.5
                                           60
10
      Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
                      25
                                        7.5
      Ala Glo Ala Glu Glo Ala Ala Thr Glo Ala Arg Ala Ala Ala Ala Ala Ala
                          5-0
                   28.85
      Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
15
                100 105 110
      Asn Arg Als Ser Leu Met Glo Leu Ile Sex Thr Asn Val Phe Gly Glo
       115 120 125
      Asa Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly Glu Met Trp
                          3.35
20
      Als Gin Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Als Ser
                       150
                                        1.55
      Ala Ser Ala Val Thr Pro Pte Ser Thr Pro Pro Glo Ile Ala Asn Pro
                                     170
      Thr Ala Gin Gly Thr Gin Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
25
                180
                                 185
                                                  196
      Ala Gly Ser Thr Ley Thr Gly Net Ile Thr Gly Leu Pro Ass Ala Leu
                             200
      Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
                          215
                                            220
30
      Trp Law Prp Glm Ile Leu Phe Cly Thr Pro Asn Phe Pro Thr Ser Ile
                      230
                                        235
      Ser Ala Leo Leu Thr Asp Leo Glo Fro Tyr Ala Ser Kaa Kaa Tyr Aso
                                         299
                    245
                                    250
      Thr Glu Gly Lew Pro Tyr Phe Ser Ile Gly Met Gly Ass Asn Phe Ile
35
                260
                                 285
      Oln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
                              280
      Val Ala Ala Ala Gly Amp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
                          293
                                           300
40
      Wet Deu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
                               315
                      310
      Val Gly Lys Leu Ser Val Fro Pro Val Trp Xee Gly Pro Leu Pro Gly
                   328
                                    330 335
      Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala
45
                                345 350
                340
      Als Pro Glu Ala Ala Pro Gly Ser Leu Leu Gly Gly Leu Pro Leu Xaz
                             360
      Bly Ala Gly Gly Ala Gly Ala Gly Pro Arg Tyr Gly Phe Xas Pro Thr
               375
                                         380
 50
      Val Met Ala Arg Pro Pro Phe Kaa Gly Ile Val Ala Ala Ala Thr Tyr
              390 395
```

(2) INFORMATION FOR SEC ID NO:127:

55

- (i) SHOUSHCE CHARACTERISTICS: (A) LENGTH: 474 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) NOLECULE TYPE: CONA
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

	OGCACGAÇCA	CCAGTTGACC	CGCGAAGAAC	CTUACCICCO	CACCCAGCGC	CGCCCGCATC	60
	ACCGGCCCCG	TCCCACGAAC	CTTTTCBGTA	AACGAGCCAC	TOCAGOGGAG	ATCGGTACCG	120
	CCCGACGCAT	TTGGTGTAAG	GACCACCTCG	COSAAGTAGT	CCTGGACGGG	TOTOCTOSOS	180
10	CCAACCAGCT	TOTAGACCETG	GCGACGGTCC	TGCTCATACT	CCACGGTUTC	TRUCTOCACO	240
	AACACCGGCC	ACATUCCTAG	TTTGCGGATG	GCCCCGATGC	COCCGGGGGGG	GGGATCACCG	300
	CGTCGCGCCC	AACTCGATTG	AGCAACGATG	GGCTTGGCCC	AGGTCGCCCA	GTTGCCACCG	360
	TCTOTCACGA	GCCGAAACAA	GGTTGCAGCC	@@CGCGCTGC	TOOTCTTSOT	GACCTOGAAC	\$20
	CAAAATTSCC	GACCCGACAT	GCGCGACTCC	CGAAACGACA	ACTGAAGCTC	GTGC	474

- (2) INFORMATION FOR SEQ ID NO:128:
  - (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1431 base pairs
    - (B) TYPE: macleic sold
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - ((i) MOLECULE TYPE: COMA

20

25.

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

	CTGCGCGCCG	GAAAAAANTA	TTACTGGCAG	GACCGGCAGA	ATGCATGGTG	ATATTCCGGT	60
	GAZGAĞĞCCĞ	CCGAGGAACC	GACTAGTGCG	AGGGTCRACA	CATCGGTTAT	TOSTTUCCOT	120
30	TTAGGTCTTU	GAT/CTGCCGG	GACGGCAACG	ACTTOGCAGO	ACCGCTCACG	CGAGCGCTGT	380
	TGACAGAGTC	GOTTCACOTC	GAACTOGCCA	CCCGTCAGAT	GCGAATGATA	GCCACATCGG	269
	CCACACCATC	GACGGCGTCG	AAGTCGCCGT	COTGGGTCAC	GACCGGCACC	CCTTGCGACG	300
	TGGCAACGGC	AGCGGCCCTC	ACCIGGACGGG	ACCUAGATCO	TCOGTGGTGT	COCCAGTUAG	360
	COTTOCGAGG	TOGOGGGTGC	AATCCCGCAT	CIGCTIGCGI	ATGCCGAAGC	COCCOCACCA	420
35	GCTCGTCTCG	ACTCAACCAT	COCCOCCOTO	COGGCTGCCT	GCOGTCAGCA	GCGCAACGGG	480
	TTTGCCGTTG	GCAGTGATGG	TGATGTCTTC	GCCGGCCTGC	ACGCGCCGTA	SCASCCCSGC	540
	GOTOTTOTTO	COCAGTICGC	GAGACGOGAC	TTCAGCAGGC	ATGCTGCGGG	GATCGGCTTU	600
	CGCTGGGCGC	GGTGTCACCG	TCATGCGCTT	GGGATATCAC	GIGATCTATC	GOCACGAAGC	669
	CGCCGGATGA	GCGAGGCAAA	COCCUTACAC	GGGCTGCCTC	GOCTTGACCG	CGCCGAACGT	726
40	TACTUTGCCG	GGGGCATCAG	CACCGTATCG	ATCATGTACA	CCGTCGCGTG	GGCGGTGTGA	780
	CTCCGCCACA	TACCAAACGG	SCOTTSTTGA	CCATGAGTCG	TOOCUGGCGC	CTATCACCGT	84.0
	CACCITÉGOCA	CCTTGCAGGT	CTGATOOGTG	COSTOSATOS	TOCTCOGACT	CGCCTGGCCG	900
	GCTATCACGT	COTAGGICAG	GATGCTGCTG	AGCAGCTTGG	COTCACTUTT	GAGTTGATCO	969
	ATAGTGGCCG	CCGGCAGCTT	GTCGAATGC3	GCSTTGGTGG	GGGCGAAAAC	SGTGTACTCS	1020
45	CCGCCGTTGA	COCTOTOGAC	CAGATTCACA	TCCOGGOTTCA	OCTTOCCOOA	CAGAGCCGAG	1089
	GTCAGGGTAC	TGAGCATCGG	GTTWTTWGGAA	GCCGCGGTAG	CGACCGGCTC	TTGCGCCATT	1146
	CCGGCCACCG	ATCCGGGACC	GGTGGGATTT	TECHCOGCGT	ATTGCGCGCA	CCCAOGACCA	1200
	ATCAGGTCCG	CTGCGGTCAG	CCATTGCCGC	CGTGGTAACG	GOCGCCGCCG	GGCTGGTCGC	1360
	COCTTTCOOG	CTGGTGTCTT	OCCACACOGG	TTTTTTTTTCTC	GAACAACCCG	CTAAGAACGC	1320
50	AATOGOGATO	OCTGOMAGGC	TOGCTGCTGC	GGCCGGTTTO	SCCTGAACGT	TGATCATCGC	1380
	TOGATION	TTGCTTCTGC	GGCGGCGTTG	AACGCCGTCC	TCCTGGGTGG	A	1631

- (2) INFORMATION FOR SHQ ID NO:129:
- (i) SEQUENCE CHARACTERISTICS:(a) LENGTH: 279 base pairs
  - (3) TYPE: nucleic acid
  - (C) STRANDEDNESS; single

(D) TOPOLOGY: linear

```
(ii) NOLECULE TYPE: CONA
 5
           (xi) SECURECE DESCRIPTION: SEC 10 NO: 129:
     SCAUSAGAGT COTATCTTTS CACCUAGUGC CUSTAGUARA CUNCTISCUT GGUTAACTUR
     GATGOGGOG GOCGTCGATT COAGAGGTAA CCGATCINCCC GCCGACAATG GCTTACCCAC
    CGAGACTMAT TGCCGCGCAG CCGCCTTCGA CGTGTAAGCC CCGGTTGGTG CATGCCGGGA 180
   ACCICTOCAC TOACUGACUT TUTACCITACIT ACCITGACGGA CITTITACGCA TUATOGCIGA
                                                                       240
     CONTETTES CICCCAGGAC TOCAGAATOT ACTOSTOCO
     (2) INFORMATION FOR SEC ID NO:130:
15
           (1) SEQUENCE CHARACTERISTICS:
             (A) LEMGTH: 1470 hase pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
70
           (ii) NOLECULE TYPE: CDMA
        (x1) SEQUENCE DESCRIPTION: SEQ ID NO:130:
25
     ACCUCCACCO GCAGCOCOGA ATCACCOTOG GTAACCTGCG AATACAATTT CTTCATCGAC 60
                                                                       130
     GACTTOGOGA ACAGCGAACC CGAGCCCACU GCCTGATAGC CTTCTTCCTC GATCTTCCAA
     CCGCCGGCGG CGTCGAACGA AACGATACGA CCCGCGCTCT GCGATCAGA CGCATGAATG 180
     TOTAGOECE CCAGCAACEG CAACECCAGC AGACCCTECA TOCCEGCGC CAGATTECCA 240
                                                                       300
     OWCACCATAA TCCCCAGCCG GTTGAFTTTG CCXXCCAAACC TCAGCGGCAC ACCCTCXAGC
     TTCTCGTAGT GCTCAAGTTC CACGGCATAC AGCCGGGCAA ACTCAACCGC GACCGCAGCC 360
30
     STOCCASCIA TOCCOGTAGO GOTGTAGTON TOCGTGATAT ACACCITGOG CACATCACGO
                                                                        420
     CUAGAAATCA TOTTGOULTO COTUGAACGC COOTCACCUG CUATGACAAC ACOGODESGO 480
     TATTICAGCO COACAANOOT OCTOCODIOC GOCAGITOCO CATCGCCGCC TGCGAGTGGC 540
     GCACCGCCGC TGATGCTTGC OGGCAGCAAC TCCGGCGCGCT GGCGGCGCAG GAAGTCAAGT 600
35
     GARAGARGAT AGGYCTACAG COGGYGTYCC AGAGAGYGAR TYRAYUGACA GGCGATCGGG
                                                                        660
     CAACOGCCAG GICACIGICO OCCCITITAG ACGIRIGOGO GGACGAAGIC CICIGOCGITO
                                                                        726
     TECTEGAGGA COTCOTEGAT TICUTUGAGE AGATOSTOGO TETECTOGOT CASCTITICO
     CUACUCTOT GUCCUUCOGC GOTGCTGCCG GCGATGTCGT CATCATCGCC GCCGCCACCG 840
     CCAGGCTTGG TCTGCTCTTG CGCCATCGCC GCCTCCTGCT TCCTCATGGC CTTTCAAAAG 980
40
     GCCGCGGGGTG COCGTCACAC GCCCGCTGTC TTTCTCTCAC CTACCGGTCA ACACCAACGT
                                                                        550
     TTCCCGGCCT AACCAGGCTT AGCGAGGCTC AGCGGTCAGT TGCTCTACCA GCTTCACGGC
                                                                        1020
     ACTOTOCACO GAATOCAGCA ACGCACCAAC ATGOGCCTTA CTACCCOGCA ACGCCTCCAG 1080
                                                                      1140
     CUTCOGGATG CERACCAGEG AGTEGEOGCE ROSTEGRAGA TERECGAGTE CORGETAGES
     GCGGCGRTRT CAGCCCCGRA COGGCGCRGG CATTICGCCG OGGRARIACG CGCGGGT9TC
                                                                       3269
45
     GGTCGGCGGF TCTCCACCGC ACTCAGCACC TGGTGTTTCG GTGACTAAAG GCTTTATCGA 1250
     DOCCOCCOCCO ACCAGCOGOT TOTACAGGCC CTTGTCCAGC CCCACATCCC AGTACTGCAG 1020
     GTTGACGAGG TWCAGCCGGG GCGCCGACCA GCTCAGGTTC TCCCGCTGCC GGAAACCGTC 1386
     GAGCAGCOGC AGTITGGCCG GCCAGTCCAG CAGCTCCGCG CAATCCATCG GGTCACGCTC
                                                                       3460
     GASCTSATCC AGCACUTGTG CCCAGGTTTC
                                                                        1470
50
     (2) INFORMATION FOR SEQ ID NO:131:
           (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1059 base pairs
55
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: Linear
```

	(ii) MOLECULE TYPE: COMA		
	(%) SEQUENCE DESCRIPTION: (	NEQ ID NO:131:	
5	ATTOCCATOS CTCCOGCACO TATCACCAGO 1	PASTOSSTT CHARGOTTT COCCOSCOCT	60
	TOCGTTGOCC TOGGCCACGO OTCGTTCATG	SOCCOTOCTS TSCSGATTSS AATTTSTSAC	120
	AACGAAATCG GGCGATCGGT GAGCAATCGT (		180
	GCCGTCAGGT SGAGTTTAGG CCAGCGTAAC A		
	ACCCACAAAC CCTGGACGCA THOSGGTUTC (		300
10	CCGATATOGG ATGCCGTAGC CITATOGAGG		360
	TECAGATGAG CTGCOGCGAC GECTGGGGCT (		420
	CATGATOROT GCCGGAATCT TIGCTCGTGC		450
	GCACGAGATT CCAATCCCCA GAAGGTCGTA		540
	OGATGATGAA COCTCTGCTC ATGCCTGCCC C		600
15	TAGCCTTGGT TCTGCATTGC ACGCGTAGGG		660
13	OTCAACAGTT TTTTTCATGC TAAGCAGATC C		730
	ECACTESTIS TOGACTACAT COTOTOGGCA (		700
	ATGCGCCAAC CGCCGTGTAG CTCGTGCCGA /		840
0.0	GACGACTACG ACGAGGCCIG GATGCTCAAC A		900
20	ARAGRAGRES TERTOCRICT COTOCCCRC 6	FTGAACAAGG AGAGGGGGCC CATCGAACTC	960
	GIAACCAAGG TAGACAAGA GGGACATCAG A	ACTOSTOTAC GATGGGGAGC CACGTTTTCA	1020
	TACAAGGAAC ATCCTAAGTT TEGATICGGG A	LACATOOTA	1059
	(2) INFORMATION FOR SEQ ID NO:132:		
25			
	(1) SEQUENCE CHARACTERISTICS		
	(A) LENGTH: 151 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
30	(D) TOPOLOGY: linear		
	(11) MOLECULE TYPE: cDNR		
	(xi) SHOURNCE DESCRIPTION: S	TWO TO WY. 122.	
35	(%E) DEGOURGE PROCEELITM: 5	ory an antinati	
22	GCACGAGGCA TTOGCOGGCA TCTGCATAAA C		60
	GAACAACATG CGATCAGAAC OFCTCCGGTG 6		129
	DETETATITE GACGACTEGE ACGACTEGIG	200	153
40	(2) INFORMATION FOR SEQ ID NO:133:		
	A second of the		
	(i) SEQUENCE CHARACTERISTICS		
	(A) LENGTH: 387 base pairs	i e	
	(B) TYPE: nucleic acid		
45			
	(D) TOPOLOGY: linear		
	(\$1) MOLECULE TYPE: cDNA		
50	(xi) SBQUENCE DESCRIPTION: S	78Q ID 80:133:	
	COGCOCOTO GATCACCGAG CCAGGCAAAR A	ATTECOMES CONTRACTOR ATTENDED	60
	CCCGGCGCAG CATCTGGCGA ACGATCACCT C		120
	GROCOCRETA GACCTCCTGG ACCTCGCGAA C		180
55	SCACCOCAS CACCICATOR SCETCSCOR A		240
Date	COTOGEC ATCOGAGAGC ACCCUTTCEG 3		300
	GCTGCCCTT GGAGATCTNG TCGTAGACCA (		360
		ITTUTUANT GOLGINGTON GGRACGATOG	
	TUATCITUTA CARCOCCTOS COGTOCT		387

	(2) IMPURMATION FOR SEQ ID NO.134:	
	(1) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 385 base pairs	
	(E) TYPE: nucleic acid	
	(C) STRANDEUNESS: Single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: CONA	
	(xi) SEQUENCE DESCRIPTION; SEQ ID NO:134:	
	GTTCAGGACG GCTATCOGAT TGYSCCGTTC GCTTCSGTGG GTGCTGAACA CGGCATCGAC	60
15	ATCHINGING ACAACGAATC CCCACTGCTG GCACCGGTCC AGTTCCTCGC CGAGAAGETG	120
	CTCGGCACCA AAGACGGTCC GGCGCTGGTC CGTGGTGTCG GACTGACACC GGTACCGCGC	180
	COCHARCOSC ASTATTACTO OFFCHOCHAS CCARCOHACA CCACAGAGTY TATUSGULAG	240
	CARGOGROU ATRACCOOCC ACCURCOONS COCCAGOCSTC COSCOSCOSC TATCGRACAC	300
	SSCRICTAGE TGATGCTGSC CRASCECCA GCCSATCCAA ATCSATCCT GGTCGGACGG	360
20	CTCTTGCDCT CSGACGCCTA AGGCGCCCC	389
	(2) INFORMATION FOR SEC ID NO:135:	
	(i) SHOUSENCE CHARACTERISTICS:	
25	(A) LENGTH: 480 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(11) MOLECULE TYPE: CDBA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO.135:	
	CORROGRATED GRATERICCO CONTROTOS COCECCIAIT TERTECTOTT GATGAGOTES	60
35	TYGGAGAAGC CYGGTTGGCG TRCCGGTWAG CCGGAATATC TYFTYGAAGC GTCACCGGAT	120
	STREACATGA ANTHONTONIN COCNOTISCOS STRITTSGRIG NGSNAAACAC GIGITIGINTA	180
	AGCCTTENTG GNCTOGNAAG NGCCQYNGAC GCCTGTGTCG CCSAAGATAA TGAGGRCYTG	240
	ACCOTTOGOO OGATOGOOCT TATOCCAAGG AATTCOGAGG TOGGTOCOGG AGATGCOGAA	300
	GOSTTOCAGO OFCTFOTTOG QUCTOTCCOG TCCCGTCACC CACTCGGCGA GGGATGTGGN	3.60
40	ACCCCCSSCG ASCSTEGCAC CAGGATCCSG CSCCSCCGCC GGAGCAGSGT CSGNNSCTGB	420
	SCTCHMITTCC TRINGCCNAA TIMBACICCN NCNACAANCI TOMMMCCCAC TCHNACCON	480
	(3) INFORMATION FOR SEQ IS NO:136:	
45	(i) SEQUENCE CHARACTERISTICS.	
	(A) LENGTH: 507 base pairs	
	(R) TYPE: nucleic soid	
	(C) STRANDEDWESS: Bingle	
	(D) TOFOLOGY: linear	
50		
	(ii) BOLECULE TYPE: CDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
55	SCACSAGGCT ACCESCECT CSCCCCCCCC GCCCTGGATG CACGCGTAGC CACCCGTNCA	-60
	THERGOGGOT CAGCOGCOC STEESGGOTT NACSCIAING CAGCTGCANA CAACOCAGOG	120
	COGGCAATTA CTTTGATGTT GAACOGATGA CCATROCCTN OGHGTHCAAT CTCNTCTCTT	180
	MCCGCGCCGC TATTIEMGCC ATAMATTIOG TINNANNCON AACGCEAGAC GTATCGAGTT	240

```
CCTTTYCGAC CACCOCCTCA ATTOTCAGCA TCCTATGGGG AACATGAGCC CCGCCGCACC 350
       GGGCGGFTTC CAAATGGTGA CDTCACAACG GTGTCACAAG CCAGCGCAAT GTCCGCGGTA 360
       GGGAGGCGGC GGCTGGGGTC GGTGGGGTGA GCSCCCGGCT TCTCAAAGGG AGGGGAGCCC
       COGGACTOTT ACCESCOGAA GEOGGOGGT STOACTGATO TAGGOTGACE GCCANNANTY
                                                                         480
       SNITHAGCCAA CAACGATGAC MACAAATAAN CCGAGGANAG ACANGNGACG GNCCGAMANG
                                                                         540
       CTNAMICCOON NUTONNONAA HEENACHCAC TYNTACCONE CTTATON
                                                                         587
      (2) INFORMATION FOR SEC ID NO.137:
10
             (4) SECUENCE CHARACTERISTICS:
               (A) LENGTH: 1200 base pairs
               (B) TYPE: mucleic soid
               (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
15
             (11) MODECULE TYPE: CDNA
             (xi) SEQUENCE DESCRIPTION: SEO ID NG: 137:
 20
     CAGGCATGAG CAGAGCETTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTACG
                                                                         120
       ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT
       TOGARARAGO COTGGREGAG CTGGCAGCAG COTTTCCGGG TGATGGCTGG TTAGGTTCGG
                                                                         130
       CUSCOGRURA ATACOCOGOC ARARACOSCA ACCACOTIGAA TITTITICCAG GARCTOGCAG
                                                                         280
       ACCTOMATOM TCAMCTEATC ACCTUATICG ACCACCAGGC CAACGCONGTE CAMACGCONACCC
                                                                         300
 25
       GCGACATCCT GGAGGGGGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC
                                                                         360
       TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCGGC CTTCCAGGCG CCGTTTTGCG
                                                                         420
       COGGCCCCAT DECONTAGTS SECCECCOCCC TTGCCTACTT SETCOTGAAA ACGCTGATCA
                                                                         489
       ACGCGACTCA ACTUCTCARA TIGCTIGCCA RATTGCGGGA GTTGGTCGGG GCCGCCATTG
       COGACATCAT TTCGGATGTO OCGGACATCA TCAAGGOCAC CCTCGGAGAA GTGTGGGAGT
     TCATCACAAA COCOCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCAGG GGGTGGGTGA
                                                                         660
       CCGGACTGTT CTCTCGAGGG TGGTCGAACC TGGAGTCUTF CTTTGCGGGC GTCCCCGGCT
                                                                        720
       TUACCESCUC GACCAGOGGC TIGTUGCAAG TUACTGGCTT GTTGGGTGCG GCCGGTCTGT
                                                                         780
       CONCATCUTC SGSCTTGGCT CACGCGGATA GCCTGGCGGG CTCAGCCAGC TTGCCCGCCC 846
       TOGOCOGCAT TOGGOGOOGG TCCCGTTTTG GOGGCTTWCC GAGCCTGGCT CAGGTCCATG
                                                                         900
 35
       COGCCTCAAC TOGGCAGGCG CTACOGCCCC GAGCTGATGG CCCGGTTGGGC GCCGCTGCCG
                                                                        960
       ASCASCIOGO COGGICANTES CASCIPOTET COGGICAGOS TICCAAGOT ATROGUCASCE 1030
       CCGTAGGCAT GGGCGGCATG CACCCCTCTT CGGGGGGGTC GAAAGGGACG ACGACGAAGA 1080
       ACGCGGGCGG TGGGCAAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GCGAGCCAA 1200
 483
      (2) INFORMATION FOR SEC ID NO:138:
             (1) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 392 amino acids
 45
               (B) TYPE: amino soid
               (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
             (ii) MCLECULE TYPE: protein
 50
             (xi) EXCURNCE DESCRIPTION: SEC ID NO.138:
       Mot Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
                      9
                                        10
 55
       Let Tyr Asp Let Let Gly Ile Gly Tle Pro Asn Gla Gly Gly Ile Let
                                     25
       Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Als Leu Glu Glu Leo Ala Ala
                                 40
```

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Als the Pro Gly Asp Gly Trp Leu Gly Ser Als Ala Asp Lys Tyr Ala
                              22
      Gly bys Asn Arg Asn His Val Asn Phe Phe Gla Glu Leu Ale Asp Leu
                         70
                                              78
 5
      Asp Arg Gin Leu fle Ser Leu fle His Asp Gin Ala Asn Ala Val Gin
                     9.49
                                          50
      Thr Thr Arg Asp Ile Leu Glu Gly Ale Lys Lys Gly Leu Glu Phe Val
                  3.50
                                      103
                                                          110
      Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
10
                                  120
                                                      123
              1:3
      Leu Ser Ala Ala Phe Gin Ala Pro Dhe Cys Ala Gly Ala Met Ala Val
                              125
                                                  340
      Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
                          150
                                              155
1.5
      Thr Gln Leu Leu Lys Leu Leu Als Lys Leu Als Glu Leu Val Als Als
                      165
                                          170
                                                              175
      Als The Als Asp The The Ser Asp Val Als Asp The The Lys Gly Thr
                  180
                                      185
                                                          190
      Leu Gly Gla Val Trp Glu Phe Ile Thr Asm Ala Leu Asm Gly Leu Lys
20
                                  200
      Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
                              215
      dly Trp Ser Asm beu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
                          230
                                              235
25
      Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                      245
                                          250
      Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Lou Ala Ser
                  260
                                      265
      Ser Ala Ser Leu Pro Ala Leu Ala Cly Ile Gly Cly Cly Ser Gly Phe
30
              275
                                  280
                                                      288
      Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Glo
          290
                              255
                                                  300
      Ale Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Glo
                          310
                                              335
      Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Mer
                      325
                                          338
                                                              335
      Gly Gly Pro Val Gly Met Gly Gly Het His Pro Ser Ser Gly Ala Ser
                  340
                                      345
                                                          350
      Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Als Als Als Gly Thr
40
              355
                                  360
      Giu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gin
                              379
      Lys Val Leu Val Arg Asn Val Val
      385
                          390
45
     (2) IMPORMATION FOR SEQ ID NO:159:
```

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 439 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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- (11) MOLECULE TYPE: CUNA
- (xi) SECUENCE DESCRIPTION: SEC ID NO:139:

ACCITIACCO ATOCCOTOGO ISCAGAGCAA COCCAGACAA CACAAACTAG TCTAATIYYO

	TTATAAAGCA GACATTTCCG TGOTTATGTA	GARGATETOS ACCGRTCAGA	TGAAGCGATC	130
	COCCTCACGT OCTATCCGAT CTCTTTTGTG	ACCATCOAGO COGTOGICTT	GGCAGCCGCG	180
	ACGOGGGACT TOCCGACGAT CGGTACCGCC	GTGAGTGCTC GGAACACAGC	COTCTGTGCC	240
	CCGACGACGG GGGTGTTACC CCCTGCTGCC	ARTGACGTOT COGTOCTSAC	@@C@@CCC@@	300
5	TICACCGCGC ACACCAAGCA CTACCGAGTG	GTGAGTAAGC CGGCCGCGCT	GGTCCATGGC	360
	ATETTOWING COCTCOCOCC GGCCACCGCC			420
	OTGOTOSCOA CCGOTTAAG			439
	(2) INFORMATION FOR SEQ ID NO:140:	*		
10				
	<ol> <li>fequence characteristic</li> </ol>	08:		
	(A) LENGTH: 1441 base pat	irs		
	(B) TYPE: macleic scid			
	(C) STRANDEDWESS: Single			
15	(D) TOPOLOGY: libear			
	(ii) MOLECULE TYPE: cDNA			
	A Real Control of the			
20	(xi) SEQUENCE DESCRIPTION:	SEC ID NO: 146:		
20			2222222	
	GAGGTTGCTG GCAATGGATT TCGGGCTTTT			60
	TTOCGGTOCG GGGCCGGAGT CGATGCTAGC			130
	OGAGTYGACT TCCGCCCCGG TCTCGTATGS			1.80
19.2	GIGGATGGGG CCGCGGCGG CCGCGATGGC			240
25	88CC9CCACG 8CG8C6CTGG CGAAGGAGAC			390
	OTTTOGGACG OCOTTCGCGA TGACGGTGCC			360
	GTTGATGTCG CTGGTCGCGG CGAACATTCT			430
	CCAGGCCBAG TATGCCGAAA TGYGGGCCCA			480
00	OSCATCIBOS SCOSCOTOS COTTOCOSCO			540
30	GOCCOGOGCCC GCGGCCGCCAG CCGCGGCGAC			600
	TGCACAGGCG ACACTGGCCC AGCTGCCCCC			660
	GGCCGCCAAC GCTGATCCGC TGACATCGGG			726
	GCAAGTCGGA TCCGCTCAGC CGATAGTGAT			780
0.0	COCCEPTAC ATTOCATION TOGOGACOGG			840
35	CAGACUCTOG CACATOGGOE TATACGGGAA			900
	TCCACTGAGT TCGGCGACCG ACGAGOCGGA			950
	GCCGGFGTCC GCGGGGGTCG GCCACGCAGC			1020
	CTGGACCACG GCCCCCCGG AGATCCAGCT			1080
***	CAGGGGGGG GCCGACGGGA CGGCCCTAAA			
40	GECTITEGOS AGOCTOSCOS CACGOSGEAC			3200
	CAGCACTGAC GGCCAAGAGG ACGGCCGCAA			1260
	OCCUCCOGA AACCCCCCC GGTAAAACTC			1330
	CCTGGTGAGC GTGGCTATCC GACGGGCCGT			
9.4	GACGACGGTG TOTGGATTCT CGGCGGCTAT	CAGAGOGATT TTGCTCGCAA	CCTCAGCRAA	1449
45	© .			1441
	(2) IMPORMATION FOR SEQ ID NO:143	3		
	(i) SEQUENCE CHARACTERISTIC			
50	(A) LENGTH: 99 amino acid			
20	(B) TYPE: amino acid	18		
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear			
	(D) TOPOLOGY: IIRest			
55	(ii) WOLECULE TYPE: protein	19		
20.00	(AA) WOMENIAM SERVE DEGREES			
	(xi) SEGUENCE DESCRIPTION:	SEC TO NO.141:		
	ment makement mentally 27000.	www. www. 1000100001		

Met Ser Phe Val Thr Tie Gin Pro Val Val Leu Ala Ala Ala Thr Gly 10 Asp Leg Pro Thr Tie Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val 20 25 Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asm Asp Val Ser 40 45 Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val 55 Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro 75 70 Ale Ale Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val 90 ala Thr Cly

1.5 (2) INFORMATION FOR SEC ID NO: 142:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 423 amino scids
- (B) TYPE: amino acid (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

85

- (ii) MOLECULE TYPE: protein 25
  - (xi) SEQUENCE DESCRIPTION: SEO TO NO:142:
- Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr 30 30 Ser Gly Pro Gly Pro Glu Ser Mot Leu Ala Ala Ala Ala Ala Trp Asp 25 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val 40
  - Val Ser Thr Leu Ile Val Glu Pro Trp Net Gly Pro Ala Ala Ala Ala 35 55 Met Als Als Als Als Thr Pro Tyr Vsl Gly Trp Leu Als Als Thr Als 26 75 Ala Len Ala Lye Glu Thr Ala Thr Gln Ala Ang Ala Ala Ala Glu Ala

90

370

- 40 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala 100 105 Aso Ary Ser Arg Leu Met Ser Leu Val Ala Ala Aso Ile Leu Gly Glo 120 125
- Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp 45 235 Ala Gin Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala 250 255 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gin Gly Thr Gly Pro
- 50 Als Gly Pro Als Als Als Als Als Thr Gln Als Als Gly Als Gly 180 285 390 Als Val Ala Asp Ala Gla Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile 200 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
- 55 215 220 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gin Val Gly Ser
  - Ala Gin Pro Ile Val Ile Pro Thr Pro Ile Gly Giu Lew Asp Val Ile

245 250 Als Leu Tyr Ile Als Ser Ile Als Thr Cly Ser Ile Als Leu Ala Ile 260 265 270 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly 4 286 285 Gly Leu Cly Pro Thr Gln Gly His Pro Leu Ser Ser Als Thr Asp Glu 295 300 Pro Glu Pro Ris Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala 310 315 10 Gly Val Gly Bis Als Als Leu Val Gly Als Leu Ser Val Pro His Ser 325 330 Trp Thr Thr Ala Ala Pro Glu Ile Gla Leu Ala Val Gla Ala Thr Pro 349 3.60 Thr Phe Ser Ser Ser Ala Cly Ala Asp Pro Thr Ala Leu Asn Gly Met 15 360 365 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg 380 370 375 Gly The Thr Gly Gly Gly Thr Arg Ser Gly The Ser Thr Asp Gly 305 306 400 20 Sin Giu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Oln Pro 405 420 425 Pro Pro Gly Asn Pro Pro Arg 420

- 25 (2) INFORMATION FOR SEC ID NO. 143:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143;
    - Net Ser Leu Leu Asp Ala His Ile Pro Glo Leu Văi Ala Ser Glo Ser 1 5 10 13
  - Ala Phe Ala Ala Lys Ala Gly Leu Met Arg Mis Thr Ile Gly Gln Ala
    20 25 25 30
    Glu Gln Ala Ala Mer Ser Ala Gln Ala Phe Hie Gln Gly Glu Ser Ser
    40 45
  - Ala Ala Phe Gin Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys 50 55 66
- 45 Val Amp Thr Leu Leu Amp Val Ala Gin Ala Amn Léu Giy Ulu Ala Ala 55 79 75 80 Gly Thr Tyr Val Ala Ala Amp Ala Ala Ala Ala Ser Thr Tyr Thr Gly 85 90 90 95
- 50 Phe

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- (2) IMPORMATION FOR SEQ ID NO:144:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

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Ala Ala Oly